

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2005, 20:37:26 / Search time 548.54 Seconds
(without alignments)
10242.778 Million cell updates/sec

Title: US-10-750-262-1
Perfect score: 1195
Sequence: 1 ccgagactccagtcagctc.....ggaaaaaaaaaaaaaaa 1195

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048.4	87.7	1050	AY403218	AY403218 Homo sapi
2	931.6	78.0	1045	AY403219	AY403219 Pan trogl
3	841	70.4	884	CA488012	CA488012 AGENCOURT
4	806	67.4	1211	AK010437	AK010437 Mus muscu
5	765.2	64.0	1050	AY403220	AY403220 Mus muscu
6	718.4	60.1	720	CA446381	CA446381 UT-H-ED1-
7	692.8	58.0	881	BG565247	BG565247 602582917
8	683.2	57.2	827	BG762026	BG762026 602718984
9	672.4	56.3	827	CV983083	CV983083 UMC-bm1x
10	672	56.2	710	BE875216	BE875216 60148516
11	663	55.5	697	DN997716	DN997716 TC115356
12	657.6	55.0	773	BU602279	BU602279 AGENCOURT
13	656.2	54.9	742	CX757709	CX757709 AGENCOURT
14	655	54.8	783	B1552907	B1552907 603197827
15	654.6	53.8	825	CX753134	CX753134 AGENCOURT
16	642.4	53.6	788	BG182296	BG182296 RST1161 A
17	640.8	53.1	788	CN153902	CN153902 941069 MA
18	640.4	53.1	799	BM995067	BM995067 UT-H-ED0-
19	634.2	53.1	799	BU930271	BU930271 AGENCOURT
20	600	50.2	600	A1686139	A1686139 tct2e11.x
21	598	50.0	609	CD677954	CD677954 ho24ho2.y
22	597.8	50.0	920	BE881257	BE881257 601492338

23	596.8	49.9	1003	3	B1551229	B1551229 603194629
24	589	49.3	1071	3	BM920324	BM920324 AGENCOURT
25	588	49.2	705	6	CB424830	CB424830 599432 MA
26	587	49.1	684	2	BE438545	BE438545 HTML-183F
27	586.2	49.1	609	5	BX103101	BX103101 BX103101
28	577.8	48.4	584	3	BM675259	BM675259 UI-E-EJ0-
29	576.2	48.2	636	6	CD690450	CD690450 EST6973 h
30	573.4	48.0	581	3	BM714075	BM714075 UI-E-EJ0-
31	559.4	46.8	891	2	BF665211	BF665211 602268114
32	554.4	46.4	581	2	BG577403	BG577403 N112 SSH-
33	553.8	46.3	773	2	BG104394	BG104394 602311010
34	550.2	46.0	779	5	BU929991	BU929991 AGENCOURT
35	534.6	44.7	661	5	BX506262	BX506262 DKFZ686E
36	521.6	43.6	600	3	B1360480	B1360480 387409 MA
37	520.8	42.2	759	6	CA509933	CA509933 UI-R-FS0-
38	499.6	41.8	705	5	BY755449	BY755449 BY755449
39	497	41.6	497	1	A1167942	A1167942 0009B06.x
40	494	41.3	1007	6	CF596595	CF596595 AGENCOURT
41	484.2	40.5	729	3	BQ211210	BQ211210 UI-R-DY1-
42	476.2	39.8	566	6	CB143042	CB143042 K-EST0196
43	475.6	39.8	654	7	CO594327	CO594327 DG3-93n7
44	474.4	39.7	686	3	BQ205543	BQ205543 UI-R-EP0-
45	472.6	39.5	1020	3	BM811413	BM811413 AGENCOURT

ALIGNMENTS

RESULT 1
AY403218
LOCUS
DEFINITION
Homo sapiens STEAP gene, VIRUAL TRANSCRIPT, partial sequence.
GENOMIC SURVEY SEQUENCE.
AY403218
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 1050)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
TITLE
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering them based on alignment.
LOCATION/Qualifiers
1..1050
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1050
/gene="STEAP"
/locus_tag="HCM1484"
ORIGIN
Query Match 87.7%; Score 1048.4; DB 10; Length 1050;
Best Local Similarity 99.9%; Pred. No. 2.1e-232;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TGGCTGAAGCCATCTATTTTATAGAAATTATGAAAAGCAGAAAAGCATCACAAACCA 95
Db 1 TGGCTGAAGCCATCTATTTTATAGAAATTATGAAAAGCAGAAAAGCATCACAAACCA 60
QY 96 GAAGAACTTTGGAAAATGAAAGCTTAGAGAAATTTAGAGAAAGCATTATTGGCATAG 155
Db 61 GAAGAACTTTGGAAAATGAAAGCTTAGAGAAATTTAGAGAAAGCATTATTGGCATAG 120
QY 156 GACACGGGAGAGACGACGATGCTAAAGAAAGACGTGTGCTTTGGATTGGCAAGAGCC 215
Db 121 GACACGGGAGAGACGACGATGCTAAAGAAAGCCTGTGCTTTGGATTGGCAAGAGCC 180
QY 216 CATGCTGATGATTTTGAATGCTGCTTCAAGAACTTCAGACACAGAGAACTCTTTCAACAG 275
Db 181 CATGCTGATGATTTTGAATGCTGCTTCAAGAACTTCAGACACAGAGAACTCTTTCAACAG 240
QY 276 TGGCACTTGGCAATTTAAATAGTGTCTATATATAGCATCTCTGACTTTTCTTACACTCTT 335
Db 241 TGGCACTTGGCAATTTAAATAGTGTCTATATATAGCATCTCTGACTTTTCTTACACTCTT 300
QY 336 CTGAGGGAAGTAATTCACCTTTAGCAACTTCCATCAACATATTTTATAAATTCCA 395
Db 301 CTGAGGGAAGTAATTCACCTTTAGCAACTTCCATCAACATATTTTATAAATTCCA 360
QY 396 ATCTGTGATCAACAAGAGCTTTGCAATGCTTTTCATCACTCTCTTGGCATTGGTTTAC 455
Db 361 ATCTGTGATCAACAAGAGCTTTGCAATGCTTTTCATCACTCTCTTGGCATTGGTTTAC 420
QY 456 CTGCCAGGTGTGATACAGCAATTTGCCAATCTTATATAGAAAGCAGATTAAGAGTTT 515
Db 421 CTGCCAGGTGTGATACAGCAATTTGCCAATCTTATATAGAAAGCAGATTAAGAGTTT 480
QY 516 CCACATTTGGTGTAGTATAGTATGTTTAAACAAGAAAGAGTTTGGGCTTCACTTCTT 575
Db 481 CCACATTTGGTGTAGTATAGTATGTTTAAACAAGAAAGAGTTTGGGCTTCTCACTTCTT 540
QY 576 TTTGCTGTACTGATCAATTTTATAGTCTGTCTTACCCAATGAGGCGATCTTACAGATAC 635
Db 541 TTTGCTGTACTGATCAATTTTATAGTCTGTCTTACCCAATGAGGCGATCTTACAGATAC 600
QY 636 AAGTGTCTAACTGGGCAATTCACAGGCTCCAAACAAATTAAGAAAGATGCTTGGATTGAG 695
Db 601 AAGTGTCTAACTGGGCAATTCACAGGCTCCAAACAAATTAAGAAAGATGCTTGGATTGAG 660
QY 696 CATGATGTTTGGAGATGAGATTTATGTCTCTGGAATTTGGGATTTGGCAATCTAG 755
Db 661 CATGATGTTTGGAGATGAGATTTATGTCTCTGGAATTTGGGATTTGGCAATCTAG 720
QY 756 GCTCTGTGCTGTGATCTATATTCATCTGTGAGTACTCTTTGAATGAGAGAAATTT 815
Db 721 GCTCTGTGCTGTGATCTATATTCATCTGTGAGTACTCTTTGAATGAGAGAAATTT 780
QY 816 CACTATATTCAGAGCAAGCTAGAGAAATTTTCCCTTCTACTGGGCAATTAACGCGATG 875
Db 781 CACTATATTCAGAGCAAGCTAGAGAAATTTTCCCTTCTACTGGGCAATTAACGCGATG 840
QY 876 ATTTTGTCTGGAATAGTATAGTATATTAACAATTTGTATGATATCACTTCAACT 935
Db 841 ATTTTGTCTGGAATAGTATAGTATATTAACAATTTGTATGATATCACTTCAACT 900
QY 936 TTTTATGATAGCTGTTTCTTCCATATTTGCTGTGATATTTAAAGCACTATTTCTG 995
Db 901 TTTTATGATAGCTGTTTCTTCCATATTTGCTGTGATATTTAAAGCACTATTTCTG 960
QY 996 CCATGCTTGAAGAAAGATGATGAGATTTAGCATGTTTGGAAAGACGTCACCAAAATTT 1055
Db 961 CCATGCTTGAAGAAAGATGATGAGATTTAGCATGTTTGGAAAGACGTCACCAAAATTT 1020
QY 1056 AACAAACTGAGATATGTTCCAGTTGTAG 1085
Db 1021 AACAAACTGAGATATGTTCCAGTTGTAG 1050

RESULT 2
AY403219 1045 bp DNA linear GSS 15-DEC-2003
LOCUS
DEFINITION
Pan troglodytes STEAP gene, VIRUTUAL TRANSCRIPT, partial sequence.
ACCESSION
AY403219
VERSION
AY403219.1 GI:39759202
KEYWORDS
GSS.
SOURCE
ORGANISM
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE
1 (bases 1 to 1045)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
Todd, M.A., Tanenbaum, D.M., Civeallo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sniinsky, J.D.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
AUTHORS
2 (bases 1 to 1045)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
Todd, M.A., Tanenbaum, D.M., Civeallo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sniinsky, J.D.,
Adams, M.D. and Cargill, M.
Direct Submision
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..1045
Location/Qualifiers
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1045
/gene="STEAP"
/locus_tag="HCM1484"
ORIGIN
Query Match 78.0%; Score 931.6; DB 10; Length 1045;
Best Local Similarity 89.4%; Pred. No. 2.7e-205;
Matches 934; Conservative 0; Mismatches 111; Indels 0; Gaps 0;
QY 41 GAAGCATCTATTTTATAGATTTAATGAAAGCAGAAAAGCATCACAAACCAAGAGA 100
Db 1 GAAGCATCTATTTTATAGATTTAATGAAAGCAGAAAAGCATCACAAACCAAGAGA 60
QY 101 ACTTGGAAATAGAGCTAGAGAAATTTAGAAAGACGATTAATTTGCATAGAGAC 160
Db 61 AATTGGANN 120
QY 161 GGGAGAGACGACATGCTAATAAAGACCTGTGCTTTGGCATTTGGCAACAAAGCCCATGC 220
Db 121 GGGAGAGACGACATGCTAATAAAGACCTGTGCTTTGGCATTTGGCAACAAAGCCCATGC 180
QY 221 TGATGAATTTGACCTGCCCTTCAGAACTTCAGACACAGAGAACTTTTCCACAGTGGCA 280
Db 181 TGATGAATTTGACCTGCCCTTCAGAACTTCAGACACAGAGAACTTTTCCACAGTGGCA 240
QY 281 CTTCGCAATTAATAATAGCTGCTATATATAGCATCTGACTTTTCTTTACACTCTTCTAG 340
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QY 341 GGAAGTAATTCACCTTTAGCAACTTCCATCAACATATTTTATAAATTCATCTCT 400
Db 301 GGAAGTAATTCACCTTTAGCAACTTCCATCAACATATTTTATAAATTCATCTCT 360
QY 401 GGTATCAACAAGCTTGGCAATGTTTCCATGACTCTCTTGGATTTGTTACTCTGCC 460

Db 361 GGTATCAACAAAGCTTCCCAATGATGTTCCATCACTCTTGGCATTGGTTTACCTGCC 420
QY AGGTGTAGTACGAGCAATTTGCCAATTCATATATGAAACCAAGTATGAAAGTATTCACA 520
Db 461 AGGTGTAGTACGAGCAATTTGCCAATTCATATATGAAACCAAGTATGAAAGTATTCACA 480
QY 521 TTGGTTGATTAAGTATGATGTTTAAACAAGCAAGTATGAGGCTTCCAGTTCTTTTTCG 580
Db 481 TTGGTTGATTAAGTATGATGTTTAAACAAGCAAGTATGAGGCTTCCAGTTCTTTTTCG 540
QY 561 TGTACTGATGCAATTTATATGCTGTCTTAAACCAATGAGGCGATCTTACATACAGTT 640
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QY 641 GCTAACTGGGCGATTCACAGGCTCCACCAAAATGAAGATGCTGATGATGAGCATTGA 700
Db 601 GCTAACTGGGCGATTCACAGGCTCCACCAAAATGAAGATGCTGATGATGAGCATTGA 660
QY 701 TGTGTGAGAAATGAGATTTATGCTCTCTGGAATTTGGAATTTGCAATACCTGCTCT 760
Db 661 GCTTTGAGAAATGAGATTTATGCTCTCTGGAATTTGGAATTTGCAATACCTGCTCT 720
QY 761 GTTGCTGTGACATCTATTTCCATCTGTGATGATCTTTGACATGAGAGAAATTCACCTA 820
Db 721 GTTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 821 TATTCAGAGCAAGCTAGGAATTTGCTTCCCTCTACTAGGCGCAATATACAGCATTTGAT 880
Db 781 NNNNNNNNAGCAAGCTAGGAATTTGCTTCCCTCTACTAGGCGCAATATACAGCATTTGAT 840
QY 881 TGCCGTGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 940
Db 841 TGCCGTGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 941 GATAGCTGTTTCTTCCCAATTTGCTGCTGATATTTAAAGCATATCTTCTGCTCATG 1000
Db 901 GATAGCTGTTTCTTCCCAATTTGCTGCTGATATTTAAAGCATATCTTCTGCTCATG 960
QY 1001 CTGAGGAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1060
Db 961 CTGAGGAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1061 AACTGATATGTTTCCCAATTTGCTGCTGATATTTAAAGCATATCTTCTGCTCATG 1085
Db 1021 AACTGATATGTTTCCCAATTTGCTGCTGATATTTAAAGCATATCTTCTGCTCATG 1045

RESULT 3
CA488012
LOCUS 884 bp mRNA linear EST 14-NOV-2002
DEFINITION AGNCOCURT_10807821 MAPL Homo sapiens cDNA clone IMAGE:6719746 5',
mRNA sequence.
ACCESSION CA488012
VERSION CA488012.1 GI:24948800
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 884)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-ide.nhl.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov

Plate: L14M14278 row: C column: 10
High quality sequence stop: 758.
FEATURES
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/organism="Homo sapiens"
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/clone="IMAGE:6719746"
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hTERT-HEM1, LNCaP"
/lab_host="EMD10B"
/clone_id="MAPL"
/note="Vector: PCMV-SPORT6, Site 1: EcoRV, Site 2: Not I;
Subcloned with brain, liver, lung, kidney and muscle.
directionally cloned, priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."

ORIGIN
Query Match 70.4%; Score 841; DB 6; Length 884;
Best Local Similarity 99.4%; Pred. No. 2.9e-184;
Matches 844; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
1 CCGAGCTCACGCTCAAGCTTAAGGCGAAGTGGGTGGCTGAAGCCATCTATTATTATAG 60
17 CCGAGCTCACGCTCAAGCTTAAGGCGAAGTGGGTGGCTGAAGCCATCTATTATTATAG 76
QY 61 AATTATGGAAGGAGAAAGACATCAACCAAGAAAGCTTTGGAAATGAAAGCTTA 120
Db 77 AATTATGGAAGGAGAAAGACATCAACCAAGAAAGCTTTGGAAATGAAAGCTTA 136
QY 121 GGAGAAATTTGAAGAGACATTTATTTGATTAAGACAGGAGAGACAGCATGCTTA 180
Db 137 GGAGAAATTTGAAGAGACATTTATTTGATTAAGACAGGAGAGACAGCATGCTTA 196
QY 181 AAAGACCTGGCTTTTGCATTTGACCAACAGCCCATGCGAATTTGACCTGCTT 240
Db 197 AAAGACCTGGCTTTTGCATTTGACCAACAGCCCATGCGAATTTGACCTGCTT 256
QY 241 CAGAACTTACGACACACAGAACTCTTTCACAGTGGCACTTGCATTTAAATAGCTG 300
Db 257 CAGAACTTACGACACACAGAACTCTTTCACAGTGGCACTTGCATTTAAATAGCTG 316
QY 301 CTATTATGACATCTGACCTTTTCTTACACTCTTCTGAGGAGATTAATCCCTTTAG 360
Db 317 CTATTATGACATCTGACCTTTTCTTACACTCTTCTGAGGAGATTAATCCCTTTAG 376
QY 361 CAACCTCCCATCAATATTTTATTAATTTCCAAATCTGCTGATCAACAAAGTCTGC 420
Db 377 CAACCTCCCATCAATATTTTATTAATTTCCAAATCTGCTGATCAACAAAGTCTGC 436
QY 421 CAATGTTTCCATCACTCTCTGCGATTTGATTAACCTGCAAGTGTATAGCAAAATG 480
Db 437 CAATGTTTCCATCACTCTCTGCGATTTGATTAACCTGCAAGTGTATAGCAAAATG 496
QY 481 TCCAACTTCATATGAGAACCAAGTATTAAGAAATTTCCAAATCTGCTGATTAAGT 540
Db 497 TCCAACTTCATATGAGAACCAAGTATTAAGAAATTTCCAAATCTGCTGATTAAGT 556
QY 541 TTAACAAGAAAGCTTTGGGCTTCTCACTTTTCTTTTGGCTGATGCAATTTATA 600
Db 557 TTAACAAGAAAGCTTTGGGCTTCTCACTTTTCTTTTGGCTGATGCAATTTATA 616
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Db 617 GTCTGCTTACCAATGAGCGATCTTACAGATTAAGTGTCTAAACTGGGCAATATCAAC 676
QY 661 AGGTCCAAACAATTAAGAAAGATGCTGATTTGAGCATGATGTTTGGAGATGAGATTT 720
Db 677 AGGTCCAAACAATTAAGAAAGATGCTGATTTGAGCATGATGTTTGGAGATGAGATTT 736

QY	721	ATGTCCTCTGGGAATTGGGATTTGGCAATCTCTGGCTCTGTGGCTCTGCATCATATTC	780		
Db	737	ATGTGCTCTGGGAATTGGGATTTGGCAATCTCTCTGTGGCTGTGCATCATATTC	796		
QY	781	CATCTGTGAGTACTCTTTTGACATGAGAGAAATTTCACTATATTTAGAGCAAGCTAGGAA	840		
Db	797	CATCTGTGAGTACTCTTTTGACATGAGAGAAATTTCACTATATTTAGAGCAAGCTAGGAA	856		
QY	841	TTGTTTCCC	849		
Db	857	ATTGTTTCC	865		
RESULT 4	AK010437	1211 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	AK010437				
DEFINITION	Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2410007B19 product:six transmembrane epithelial antigen of the prostate, full insert sequence.				
ACCESSION	AK010437	GI:12845880			
VERSION	AK010437.1	GI:12845880			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	Carninci, P. and Hayashizaki, Y.				
AUTHORS	1				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, T., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujimake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsui, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
PUBMED	11076661				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
PUBMED	5				
REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
JOURNAL	Nature 420, 563-573 (2002)				
PUBMED	6 (bases 1 to 1211)				
REFERENCE	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Aikawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y.,				

TITLE

JOURNAL

Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer 15' GAGAGAAGAGATCCCAAGACCTCTTTTCTTTTTTNN 3'), cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence 15' GAGAAGAAATTCTCGAGTTAATTAAATTAATCCCCCCCCC 3'). cDNA was cleaved with XhoI and SacI. Cloning sites, 5' end: XhoI; 3' end: SacI.

Host: SOLR.

FEATURES

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ORIGIN

Query Match	67.4% Score 806 DB 4: Length 1211;
Best Local Similarity	81.0%; Pred. No. 4e-176; Indels 4; Gaps 1;
Matches 952; Conservative 0; Mismatches 220;	

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      3   GAGACTACCGTCACAGCTTAGCGGAAGAGTGGGTGCCTGAAGCCATACTATTTTATAGAA 62
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      35 GCgcctgCGcgtGcggrGCCAcGGAAGAgccGsgtGcTGAAGCcGrATATTTTATnGCA 94

      63 TTATGGAAGACGAAAAGACATCACAAACCAAGAACTTTGGAAAAATGAAGCTTAG 122
Db       |          |||||              |||||              |||||              |||||
      95 GTCATGAGAGATCAgTgCGATgTTAACAAACCAGAAcCACTTTGGAAAAATGAAGCCAAAG 154

      123 AGAAATTTAAGAGAGCATTTATTTGGCAATAGGACACGGGAGAGACCAAGCATCTAAAA 182
Db       |          |||||              |||||              |||||              |||||
      155 GGAACCTGGAAGATGCAgTACTGCACTTAAGGACCTCGGAGAGAGACAGACATGCTGAAA 214

      183 AGACCTGCTGCTTTGGACTTTGGACCAAAcAGCCcATGCTGATGAATTTGACTGcCCCTTCA 242
    
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Db	215	AGACCGGGGCTCGCACTTGCAGCAGCGGGTCAAGTGGATGCCCTTTGACTGCCCTCC	274
Qy	243	GAACCTCAGCACACAGGAACCTTTCCACAGTGGCACTTGGCAATTAAATAGCTGCT	302
Db	275	GAGCTTCACACACGAGGAAATCTTCCAAATCGCGCTTGGCAATGAAGTCGTGCC	334
Qy	303	ATTATAGCATCTCTGACTTTTCTTACACTCTCTGAGGGAAGTAATACCCCTTAGCA	362
Db	335	ATCATATATATCCCTGACTTTCTCTGACACACTTCTAGGGAATCATACCGCTTAGTA	394
Qy	363	ACTTCCCATCAACAAATATTTTATTAATAATTCAAATCTGCTCATCAACAAAGCTTGGCA	422
Db	395	ACCTCCCGTGAACAAATATTTTATTAATAATTCAAATCTGCTTAGTAACAAAGCTTGGCA	454
Qy	423	ATGGTTCCATCACTCTTGGATATGTTTACCTGCGAGGTGTATATACAGAAATTCG	482
Db	455	ATGGTGGCCATTAACCTCTTGGACTGGCTATATTTGCCAGGAAGTTACCGGAGTTGTA	514
Qy	483	CAACTTCATATATGAACCAAGTATATGAAGTTTCCATTTGGTTGATATAGATGTTA	542
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Qy	543	ACAAAGAAAGCACTTTGGGCTTCTCACTTTCTTTTGTCTGTACTGATGCAATTTATAGT	602
Db	575	GCCAAAGAAAGCAATTTGGTCTCTCCACAGCTTCTTTTGTCTGTCTGCAACCTGTATTACAT	634
Qy	603	CTGTCTTACCAATGAGGCGATCTCATACATCAAGTTGCTTAACTGGGCTATATCAAG	662
Db	635	CTCTCATACCAATGAGGAGATCTTACAGATACAGCTACTCAACTGGGCTTACCAACG	694
Qy	663	GTCCAACAAAATPAAAGAGATGCTGTGATTTGAGCATGATGTTTGGAGAAATGAGATTAT	722
Db	695	GTTCAACAAACAAAGAGATGCTGTGATTTGAGCATGATGTTTGGAGAAATGAGATTAT	754
Qy	723	GTGTCTCGGGAATTGTGGGATTTGGCAATACGCGCTGTGGCGTGTGACATCTATTCOA	782
Db	755	GTGTCTCGGGAATTGTGGGCTGTGGCAATCTTGGCTCTCTTGTGGTGTGACATCTATTCOA	814
Qy	783	TCTGTAGTGAATCTTTTGACATGAGAGAAATTTCACTATTTACAGAGCAAGCTAGGAAT	842
Db	815	TCTGTAGTGAATCTTTTAACTGAGAGAAATTTCACTATTTACAGAGCAATAGGAAT	874
Qy	843	GTTCCTCTTCTACTGGGCAATACACGATTTGATTTTGTGCTGGATATAGTGATAGAT	902
Db	875	GTCTCTCTCTCTGTGGGCAATACACGATTTGATTTTGTGCTGGATATAGTGATAGAT	934
Qy	903	ATPAAACAAATTTGTATGTATACATCTCCAACTTTTATATGATATGCTTTCTTCCAAAT	962
Db	935	GTCACTCAATTTGTATGTATACATCTCCAACTTTTATATGATATGCTTTTCTTCCAACT	994
Qy	963	GTGTCTGTATATTTAAAGCATACTATATCTTGGCATGCTTGGAGAAAGATACTGAAG	1022
Db	995	CTGTCTGTATATTTAAAGCATCTCTGTGGCATGCTTGGAGAAAGATACTGAAG	1054
Qy	1023	ATTAGACATGTTGGGAGACGTCCAAATTAACAAACCTGATATATGTTCCAGTTG	1082
Db	1055	ATTAGATGTGTGGGAGATGTCCAAATTAACAGACTGATGATGCTCCAGTTG	1114
Qy	1083	TAGATTTACTGTTTACACACTTTTGTTCATATTTGATATATTTATCCACCAATTC	1142
Db	1115	TAGACATCTGTTTGCACATATTTGCTGTTAT----TGAATCTCATATATAGATTTTC	1170
Qy	1143	AAAGTTGATTTGTTAATTAATATGTTATTCAGGA	1178
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RESULT 5	AY403220	1050 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY403220				
DEFINITION	Mus musculus STEAP gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				

Accession	AY403220
Version	AY403220.1 GI:39759203
Keywords	GSS.
Source	Mus musculus (house mouse)
Organism	Mus musculus
Reference Authors	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
Title	1 (bases 1 to 1050)
Journal	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
PubMed	2 (bases 1 to 1050)
References	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Authors	Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Title	Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Journal	Adams,M.D. and Cargill,M.
Comment	Adams,M.D. and Cargill,M.
Features	Inferring nonneutral evolution from human-chimp-mouse orthologous
Source	gene tinos
Location/Qualifiers	Science 302 (5652), 1960-1963 (2003)
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organism	1.1050
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db_xref	/mol_type="genomic DNA"
gene	<db_xref="taxon:10090"
locus_tag	<1.1050
locus_tag	/gene="STEAP"
locus_tag	/locus_tag="NCM1484"
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Best Local Similarity	83.0%; Pred. No. 1,1e-166;
Matches	872; Conservative 0; Mismatches 178; Indels 0; Gaps 0;
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Qy	36 TGGCTGAAGCCATCACTATTATTAGAAATTAAGAAAGAGAAAGACATCAACAAACCA 95
Db	1 TGGCTGAAGCCATCACTATTATTAGAAAGATCAAGAGATCAAGAGATTAACAAACCA 60
Qy	96 GAAGAACTTTGAAAATGAAGCTTGAAGAAATTTAGAAAGAGATTAATTGCAATAG 15
Db	61 GAACAACTTTGAAAATGAAGCCAAAGGAAACCTGGAAGATGACAGTTACTCGACTAG 120
Qy	156 GAAACGGAGAGACCGAGCATGCTAAAGAAAGCCTGCTTTGGCAATTGCACAAACGCC 215
Db	121 GACTCGGAGAGACGAGCATGCTAAAGAAAGCCGGGGCTCTGCACCTTGACAGACGGGTC 180
Qy	216 CATGCTGATGAATTTGACTGACCTTCAGAACTTCAGACACAGAACTTTCCACAG 275
Db	181 CAGGTGATGCTTTGACTGACCTTCAGAACTTCAGACACAGAACTTTCCCAAC 240
Qy	276 TGGCACTTGGCAATTAATAGCTGCTATTAATAGCATCTTGACTTTCTTTACACTTT 333
Db	241 TGGCGCTTCCACAGTGAAGTCCGCTCCATCATATCATCCCTGACCTTCTGTACACACTT 300
Qy	336 CTGAGGGAAGTATTAACCCCTTTACCACTTCCCACTCAAACTAATTTTATTAATTCGA 399
Db	301 CTGAGGGAAGTATTAACCCCTTTAGTAACTTCCGCTGAACAATTTTATTAATTCGA 360
Qy	396 ATCTGTGATCAACAAGCTTTGGCAATGGTTTTCATCACTCTCTTGGCAATGGTTTAC 455
Db	361 ATCTGTGATTAACAAGCTTTGGCAATGGTTCATTAACCTCTTGGCAATGGTTCAT 420
Qy	456 CTGCGAGGTGTATAGACAGCAATTTGCCAATTTCAATATGAAACCAAGTATGAAGTTT 515
Db	421 TTGCGAGGAGATTTGCGCAGTTGTATACGCTTGGCAATGAAACCAAGTATGAAGTTT 480

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QY 516 CCACATGGTGGATGAATGATGATGATTAACAGAAAGAGTTGGCTTCTCAGTTCTTT 575
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QY 576 TTTGCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 635
DB 541 TTTGCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 636 AAGTGGCTAAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 695
DB 601 AAGTGGCTAAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 696 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 755
DB 661 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
QY 756 GCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 815
DB 721 GCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 816 CACTATATTCAGAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 875
DB 781 CACTATATTCAGAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 840
QY 876 ATTTTGGCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 935
DB 841 GTTTTGGCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 936 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 995
DB 901 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
QY 996 CCATGCTGAGAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1055
DB 961 CCTGCTGAGAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1020
QY 1056 AACAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1085
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RESULT 6
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LOCUS UI-H-EDI-axr-o-23-0-UI.s1 NCI CGAP EDI Homo sapiens cDNA clone
DEFINITION UI-H-EDI-axr-o-23-0-UI 3', mRNA sequence.
ACCESSION CA446381
VERSION CA446381.1 GI:24810801
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 720)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

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FEATURES
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1..720
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/mol_type="mRNA"

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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP EDI"
/note="Organ: Left Pubic Bone; Vector: pRT73-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP EDI is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C55. The library was constructed according to
Bonfido, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pRT73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
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TAG_LIB=UI-H-EDI
TAG_SEQ=CGTCAAGGCT"

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ORIGIN

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Query Match 60.1%; Score 718.4; DB 6; Length 720;
Best Local Similarity 99.9%; Pred. No. 8e-156;
Matches 719; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 476 AATGTCGAACCTTCAATATGGAACCAAGTATAGAAGTTCCACATGTTGGATGAATG 535
DB 720 AATGTCGAACCTTCAATATGGAACCAAGTATAGAAGTTCCACATGTTGGATGAATG 661
QY 536 GATGTTAAACAAGAAAGAGTTGGCTTCTCAGTTCTTTTGGCTGATGATGAT 595
DB 660 GATGTTAAACAAGAAAGAGTTGGCTTCTCAGTTCTTTTGGCTGATGATGAT 601
QY 596 TTTATGCTGTTTACCCATGAGCCGATCTCTACGATACAAAGTCTAAATCGGGCATA 655
DB 600 TTTATGCTGTTTACCCATGAGCCGATCTCTACGATACAAAGTCTAAATCGGGCATA 541
QY 656 TCACAGAGTCCCAACAAATTAAGAGATGCTGATGATGATGATGATGATGATGATGATG 715
DB 540 TCACAGAGTCCCAACAAATTAAGAGATGCTGATGATGATGATGATGATGATGATGATG 481
QY 716 GATTTATGCTGCTGAGGAATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 775
DB 480 GATTTATGCTGCTGAGGAATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 421
QY 776 TATTCATCTGAGTGAATCTTTTGAACATGAGAGAAATTTCACTATATTCAGAGCAAGCT 835
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DB 360 AGGAATGTTTCCCTTCTCACTGGGCAATACAGCCATGATTTTGGCTGGAATAGTG 301
QY 896 GATGATATTAACAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 955
DB 300 GATGATATTAACAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 241
QY 956 TCCATGTTGTCCTGATATTTTAAAGCATATCTTCCGATGCTTGAAGAAAGAT 1015
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DB 180 ACTGAAGATTAAGACATGTTGGAGAGCTCACCAAAATTAACAAACTGAGATATGTC 121
QY 1076 CCAGTTGTAAGATTAAGTATTAACACATTTTGTCAATATGATATATTTATCACA 1135
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 RESULT 7
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 DEFINITION mRNA sequence. 881 bp mRNA linear EST 10-Apr-2001
 ACCESSION BG565247
 VERSION BG565247.1 GI:13572900
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LNCM1549 row: b column: 05
 High quality sequence stop: 704.

FEATURES
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 /clone_lib="NIH_MGC_76"
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 sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.85
 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 58.0%; Score 692.8; DB 2; Length 881;
 Best Local Similarity 92.0%; Pred. No. 7.2e-150;
 Matches 786; Conservative 0; Mismatches 62; Indels 6; Gaps 5;
 QY 251 GCACACAGAGAACTCTTTCCAGAGGCGACTTGGCAATTAATAGCTATTATAGC 310
 Db 1 GCACACAGAGAACTCTTTCCAGAGGCGACTTGGCAATTAATAGCTATTATAGC 60
 QY 311 ATCTGACTTTCTTTTACACTCTTCTGAGGAGAAATATACCCCTTTAGCACTTCCCA 370
 Db 61 ATCTGACTTTCTTTTACACTCTTCTGAGGAGAAATATACCCCTTTAGCACTTCCCA 120
 QY 371 TCACACATATTTTATTAATTAATTCATCTGTCATCAACAAGCTTGGCAATGTTTC 430
 Db 121 TCACACATATTTTATTAATTAATTCATCTGTCATCAACAAGCTTGGCAATGTTTC 180
 QY 431 CATCACTCTTGGCAATGTTTACTGCGAGGTGATAGAGCAATGTCCAACTTCA 490
 Db 181 CATCACTCTTGGCAATGTTTACTGCGAGGTGATAGAGCAATGTCCAACTTCA 240

QY 491 TAATGACCAAGTATTAAGAGTTTCCACATTTGGTGGATTAAGTATGTTAAAGAAA 550
 Db 241 TAATGACCAAGTATTAAGAGTTTCCACATTTGGTGGATTAAGTATGTTAAAGAAA 300
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 Db 301 GCAAGTTGGGCTTCTCAGATTTCTTTTGGCTGATGCAATGCAATTAATAGTCTCTTA 360
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 Db 361 CCCAATGAGGCGATCTTACAGATTAAGTTGCTAAACCTGGGCAATCAACAGTCCAAAC 420
 QY 671 AATAAAGAAGATCCCTGATTTAGCATGATGTTTGGAGAAATGAGATTTATGTCTCT 730
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 Db 481 GGGAAATTTGGGATTTGG-ATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTAG 539
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 Db 540 TGACTCTTTGACATGAGAGAAATTTCACTATATTCAGACCAAGCTTGAATGTTCCCT 599
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 QY 969 CTGATATTT-AAAAGATCTATT--CCGCCATGCTTGGAGAAAGATAC- GAAGAT 1025
 Db 720 CTGATATTTCAAACGATACATATCTTACCTGCAAGCTTGAAGAGAAATACAGAGATT 779
 QY 1026 AGACATGTTGGGAGAGACCTCAACCAAAATTAACAAACAGATATGTTCCAGTTGTAG 1085
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 QY 1086 AATTACTGTTTACA 1099
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 LOCUS BG762026
 DEFINITION mRNA sequence. 961 bp mRNA linear EST 15-May-2001
 ACCESSION BG762026
 VERSION BG762026.1 GI:14072679
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DC/DTP
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LNCM1713 row: b column: 21
 High quality sequence stop: 750.

Instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of poly(A)⁺ RNA was annealed at 37 degrees with 10mcg of NotI-tag-dT18 oligonucleotide (GCTGCTGGGGCGC-tag-T18) and reverse transcribed at 37 degrees with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (<http://genome.utoronto.edu/pubsoft/softwares.html>) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and Kase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life Technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10 bacteria. Preliminary library characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (-4-96-well plates) to confirm library quality [e.g. the presence of short polyA tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's bioinformatics group in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@net.missouri.edu. Citations: Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Dillon BA, Mathalagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(da) tails. Biotechniques 31:38-42. Soares MB, MF Bonaldo, P Jelene, L Su, L Lawton, A Efstratiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232. TAG TRISUB=Conceptus-Corpus Luteum (mixed) TAG_SEQ=Not Found

ORIGIN

Query Match 56.3%; Score 672.4; DB 8; Length 827;
 Best Local Similarity 89.3%; Pred. No. 3,9e-145;
 Matches 735; Conservative 0; Mismatches 87; Indels 1; Gaps 1;

QY 1 CCGAGACTACGCTCAAGCTTAAGCGGAGAGTGGTGGCTGAAGCCATCTATTATTATAG 60
 DB 5 CCGCACTTACGCTCAGCTCAGCAAGAGCGGGTGGCTGAAGCCATCTATTATTATAG 64
 QY 61 AATT-ATGGAAGCAAGAAAGACATCAACCAAGAAACTTTTGGAAATGAAGCCT 119
 DB 65 AATTAAATGAGAGCAAGACATCAACCAAGAAACTTTTGGAAATGAAGCCT 124
 QY 120 AGGAGAAATTTAGAGAGAGATTATTTGATTAAGAGACCGGAGAGACCATGCTTA 179
 DB 125 AGGAGAAATCTTAAGAGAGATGATTTATTAAGAGATCAAGAGAGATCGGACATGCT 184
 QY 180 AAAAGACCTGTGCTTTTGCATTGGACCAACGACCCATGCTGATGAATTGACTGCCT 239

DB 185 AAAAGACATGTGCTTTTGCATTGGACCAACCAACCATTTTGATGAATTGATGCCCC 244
 QY 240 TCAGACTTCAGACACACAGAGAACTCTTCCAGAGGCACTTGGCAATTAATAGCT 299
 DB 245 CCGAGCTTCAGAGAAACAGAAACCTTTCCAAAGTGGCGCTTGGCAATTAATAGCC 304
 QY 300 GCTATTATAGCATCTGCACTTTCTTTTCACTCTTTCTGAGGGAAGTAATTCACCTTTA 359
 DB 305 GCTATTATGATCATCTGCACTTTCTTTCTCACTCTTGTAGGGAATTAATTCACCTTTT 364
 QY 360 GCACTTCCCATCAACATTTTATTAATTTCAATCTGTCTATCAACAAAGCTTG 419
 DB 365 GTGACTTCCCATCAACAGATTTTAAATTTCAATCTGTCTATCAACAAAGCTTG 424
 QY 420 CCAATGTTTCCATCACTCTTGGCATTGGTTTACCTGCAAGTGTAGAGCAAT 479
 DB 425 CCAATGTTTCCATCACTCTTGGCATTGGTTTATTTGCAAGTGTAGAGCAAT 484
 QY 480 GTCCAACTTCATTAATGAACCAAGTAAAGATTTCACATTTGATTAAGTGAAT 539
 DB 485 GTGACACTTCATTAATGAACCAAGTAAAGATTTCGACATGTTGATGATGATG 544
 QY 540 TTAACAAGAAAGCATTTGGGCTTCTCACTTTCTTTTGTGCTGATGCAATTTAT 599
 DB 545 GTAAACAAGAAAGCATTTGGTCTTCTCACTTTCTTTTGTGCTGATGCAATTTAT 604
 QY 600 AGTCTGCTTCAACCAATGAAGGATCTCACTGATTAAGTGTGTAATGGGCAATTC 659
 DB 605 AGTTTATCTTATCCATGAAGGATCTCACTGATTAAGTGTGTAATGGGCAATTC 664
 QY 660 CAGGTCCAAACAAATTAAGAAAGTGCCTGATTTGAGCATGATTTGGAATGAGATT 719
 DB 665 CAGGTCCAAACAAATTAAGAAAGTGCCTGATTTGAGCATGATTTGGAATGAGATT 724
 QY 720 TATGTCTCTGGAATTTGGGATTTGCAATTAAGTGTGCTGTGATCTATT 779
 DB 725 TATGTATCACTGGGAATCTGGACACTTGAATTAAGTGTGCTGTGATCTATT 784
 QY 780 CCATCTGTAGTGAATCTTTGACATGAGAGAAATTTCACTATA 822
 DB 785 CCATCTGTAGTGAATCTTTGACATGAGAGAAATTTCACTATA 827

RESULT 10
 BE875216 710 bp mRNA linear EST 20-OCT-2000
 LOCUS BE875216
 DEFINITION 601488516P1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:389030 5',
 mRNA sequence.
 ACCESSION BE875216
 VERSION BE875216.1 GI:10323992
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 710)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>,
 TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTP/Gazdar
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.llnl.gov>
 Plate: L1M9674 row: p column: 03
 High quality sequence stop: 701.
 Location/Qualifiers
 1. 710

FEATURES
 source

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE 1 (bases 1 to 742)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Meri Firpo
 cDNA Library Preparation: Express Genomics
 cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM115916 row: h column: 13
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 High quality sequence stop: 726.
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 /clone="IMAGE:7772991"
 /tissue_type="pluripotent cell line derived from
 blastocyst inner cell mass"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_278"
 /note="Organ: Blastocyst; Vector: pExpress-1; Site_1:
 EcoRV; Site_2: NotI; RNA obtained from pluripotent cell
 line derived from blastocyst inner cell mass (cell line
 HSF-1.14, NIH Registry designation UCO1. Positive for OCT4
 expression by rtPCR, positive for SSEA-3, SSEA-4,
 TRA-1-81, TRA-1-60 by immunofluorescence. Negative for
 SSEA-1 by immunofluorescence. Passage 35. This line is a
 subclone of the parental line; the parental line was
 subcloned to remove aneuploid cells). cDNA was primed
 using oligo-dT primer:
 5'-pGACTGTTCTGATGTCGAGCGGCGGCC(T)25-3' and cloned into
 the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
 kb resulted in an average insert size of 1.9 kb. This
 primary library is non-normalized (normalized primary
 library is NIH MGC 279) and was constructed by Express
 Genomics (Frederick, MD). Note: this is a Mammalian Gene
 Collection library."

ORIGIN
 Query Match 54.9%; Score 656.2; DB 8; Length 742;
 Best Local Similarity 97.4%; Pred. No. 2.2e-141;
 Matches 667; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

1 CGAGACTCAGCGTCAAGCTTAAGCGAAGGTGGTGGTGAAGCACTATTATTATG 60
 |
 58 CTGAGACTACGGTCAAGCTACGCGAGGAGTGCGTGAAGCCACTATTATTATG 117
 |
 61 AATTATGGAAGCAGAAAAGACATCAACAACCAAGAGAACTTTGGAAATGAAGCTT 120
 |
 118 AATTATGGAAGCAGAAAAGACGTCACAAACCAAGAGAAATTTGGAAATGAAGCTT 177
 |
 121 GGAGAAATTTAGAGAGAGAGAGATTTATTCATTAAGACACGGAGAGACACAGATGCTAA 180
 |
 178 GGAGAAATTTAGAGAGAGAGAGATTTATTCATTAAGACACGGAGAGAGACAGATGCTAA 237
 |
 181 AAAGACTGTGCTTTGCAATTTGACCAACAGCCCATGCTGATGATTTGACTGCCCTT 240
 |
 238 AAAGACTGTGCTTTGCAATTTGACGAGAAACGCCCATGCTGATGATTTGACTGCCCTT 297
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241 CAGAACTTCAGCACACACAGAAACTCTTTCCAGAGTGGCACTTGCCATTTAAATAGCTG 300
 |
 298 CAGAACTTCAGCACACACAGAAACTCTTTCCAGAGTGGCACTTGCCATTTAAATAGCTG 357
 |
 301 CTATTATGACATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTATTCACCTTTAG 360
 |
 358 CTGTTATGCAATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTATTCACCTTTAG 417
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 361 CAATCCCATCAACAAATATTTTATAAATTCATCTGCTGTCATCAACAAATCTTGC 420
 |
 418 CAATCCCGGCAACAAATATTTTATAAATTCATCTGCTGTCATCAACAAATCTTGC 477
 |
 421 CAATGTTTCATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTATTCACCTTTAG 480
 |
 478 CAGGTTTCATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTATTCACCTTTAG 537
 |
 481 TCACACTCATATGGAACCAAGATATGAAGTTTCCACATTTGATGATGATGT 540
 |
 538 TCACACTCATATGGAACCAAGATATGAAGTTTCCACATTTGATGATGATGT 597
 |
 541 TAACAGAAAGCAGTTGGGCTTCAGTTCTTTTCTGTTACTGATGCAATTTATA 600
 |
 598 TAACAGAAAGCAGTTGGGCTTCAGTTCTTTTCTGTTACTGATGCAATTTATA 657
 |
 601 GTCTGTTTACCCATGAGGCGATCTCTACATCAAGTTGCTTAACTGGGCAATATCAAC 660
 |
 658 CTCTGTTTACCCATGAGGCGATCTCTACATCAAGTTGCTTAACTGGGCAATATCAAC 717
 |
 661 AGGTCAACAAATATTAAGAGATGC 685
 |
 718 AGGTCAACAAATATTAAGAGATGC 742
 |

RESULT 14
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 LOCUS 60319782721 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5277295 5',
 DEFINITION mRNA sequence.
 ACCESSION B1552907 GI:15440219
 VERSION B1552907.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE 1 (bases 1 to 783)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Miklos Pal Kovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM11700 row: e column: 08
 High quality sequence stop: 769.
 Location/Qualifiers
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 /clone_lib="NIH_MGC_95"
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 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI

(gtagag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTT-3', size-selected for average
insert size 2.5 kb and normalized to R0T 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

ORIGIN

Query Match 54.8%; Score 655; DB 3; Length 783;
Best Local Similarity 99.0%; Pred. No. 4.2e-141;
Matches 680; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

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QY 1 CCGAGACTCAGCGTCAAGCTAAGCGGAGAGTGGTGGTGGAGCCATCTATTATTAG 60
DB 97 CCGAGACTCAGCGTCAAGCTAAGCGGAGAGTGGTGGTGGAGCCATCTATTATTAG 156
QY 61 AATTAATGGAAGCAGAAAAGATCAACAACCAAGAACTTTGGAATGAGCCTA 120
DB 157 AATTAATGGAAGCAGAAAAGATCAACAACCAAGAACTTTGGAATGAGCCTA 216
QY 121 GGAAGAAATTTGAAGAAAGAGATTTTGCATTAAGACACGGAGAGACCAAGATGCTAA 180
DB 217 GGAAGAAATTTGAAGAAAGAGATTTTGCATTAAGACACGGAGAGACCAAGATGCTAA 276
QY 181 AAGAGCTGTGCTTTTGCATTTGCAACCAAGCCCAAGTGTGAATTTGACCTGCTT 240
DB 277 AAGAGCTGTGCTTTTGCATTTGCAACCAAGCCCAAGTGTGAATTTGACCTGCTT 336
QY 241 CAGAACTTCAGACACACAGAACTCTTTCACAGTGGCAGCTTCCCAATTAATAGCTG 300
DB 337 CAGAACTTCAGACACACAGAACTCTTTCACAGTGGCAGCTTCCCAATTAATAGCTG 396
QY 301 CTATTATAGCATCTCTGACTTTTCTTTTACCTCTTTCAGGAAATTAATCACCCTTAG 360
DB 397 CTATTATAGCATCTCTGACTTTTCTTTTACCTCTTTCAGGAAATTAATCACCCTTAG 456
QY 361 CAAGTCCCATCAACAATATTTTATTAATTCACATCCGATCATCAACAAGTCTGTC 420
DB 457 CAAGTCCCATCAACAATATTTTATTAATTCACATCCGATCATCAACAAGTCTGTC 516
QY 421 CAATGTTTTCATCACTCTCTTGGCATTTGGTTTACCTGCGAGTGTGATAGCAGCAATTG 480
DB 517 CAATGTTTTCATCACTCTCTTGGCATTTGGTTTACCTGCGAGTGTGATAGCAGCAATTG 576
QY 481 TCCAACTTATTAATGGAACCAAGTATTAAGAGTTTCCACATTTGTTGATAGTGAATG 540
DB 577 TCCAACTTATTAATGGAACCAAGTATTAAGAGTTTCCACATTTGTTGATAGTGAATG 636
QY 541 TAAACAAGAAAGAGTGGGCTTCTCAGTTTCTTTTCTGCTGATGCA-TGCAATTTAT 599
DB 637 TAAACAAGAAAGAGTGGGCTTCTCAGTTTCTTTTCTGCTGATGCA-TGCAATTTAT 696
QY 600 ACTCTGTCTTACCCATGAGGCGATCTCAGATATAGATGCTTAACCT-GGGCATATATCA 658
DB 697 ACTCTGTCTTACCCATGAGGCGATCTCAGATATAGATGCTTAACCT-GGGCATATATCA 756
QY 659 AAGAGTCCAAACAAATTAAGAAAGATGC 685
DB 757 CCAAGTCCAAACAACTACCAAGATGC 783

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RESULT 15

LOCUS CX753134 825 bp mRNA linear EST 24-JAN-2005
DEFINITION AGENCOURT 40991781 NIH_MGC 281 Homo sapiens cDNA clone
IMAGE:7780881 3', mRNA sequence.
ACCESSION CX753134
VERSION CX753134.1 GI:58049789
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 825)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: Meri Firpo
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
<http://image.llnl.gov>
plate: LLAM15937 row: a column: 07
High quality sequence stop: 538.
Location/Qualifiers

FEATURES

Source

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7780881"
/isue_type="pluripotent cell line derived from
blastocyst inner cell mass"
/lab_host="DH10B Tena"
/note="Organ: Blastocyst; Vector: pExpress-1; Site:1;
EcorV, Site 2: NotI; RNA obtained from pluripotent cell
line derived from blastocyst inner cell mass (cell line
HSF-6, NIH Registry designation UC06. Positive for OCT4
expression by RT-PCR, positive for SSEA-3, SSEA-4,
Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
SSEA-1 by immunofluorescence Passage 62. cDNA was primed
using oligo-dT primer:
5'-pGACTGTTCTGATGCGAGGCGGCGCCCT(7)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
kb resulted in an average insert size of 2.0 kb. This
primary library is normalized (non-normalized primary
library is NIH_MGC 280) and was constructed by Express
Genomics (Frederick, MD). Note: this is a Mammalian Gene
Collection library."

ORIGIN

Query Match 54.8%; Score 654.6; DB 8; Length 825;
Best Local Similarity 98.5%; Pred. No. 5.2e-141;
Matches 671; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

```

QY 1 CCGAGACTCAGCGTCAAGCTAAGCGGAGAGTGGTGGTGGAGCCATCTATTATTAG 60
DB 65 CCGAGACTCAGCGTCAAGCTAAGCGGAGAGTGGTGGTGGAGCCATCTATTATTAG 124
QY 61 AATTAATGGAAGCAGAAAAGATCAACAACCAAGAACTTTGGAATGAGCCTA 120
DB 125 AATTAATGGAAGCAGAAAAGATCAACAACCAAGAACTTTGGAATGAGCCTA 184
QY 121 GGAAGAAATTTGAAGAAAGAGATTTTGCATTAAGACACGGAGAGACCAAGATGCTTA 180
DB 185 GGAAGAAATTTGAAGAAAGAGATTTTGCATTAAGACACGGAGAGACCAAGATGCTTA 244
QY 181 AAGAGCTGTGCTTTTGCATTTGCAACCAAGCCCAAGTGTGAATTTGACCTGCTT 240
DB 245 AAGAGCTGTGCTTTTGCATTTGCAACCAAGCCCAAGTGTGAATTTGACCTGCTT 304
QY 241 CAGAACTTCAGACACACAGAACTCTTTCACAGTGGCAGCTTCCCAATTAATAGCTG 300
DB 305 CAGAACTTCAGACACACAGAACTCTTTCACAGTGGCAGCTTCCCAATTAATAGCTG 364
QY 301 CTATTATAGCATCTCTGACTTTTCTTTTACCTCTTTCAGGAAATTAATCACCCTTAG 360

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Db 365 |||||CTATTATGCACTCTGACCTTTCTTTACCTCTTGAGGGAAGTAATTCACCCCTTAG 424
Qy 361 |||||CAACTTCCGATCAACAATATTTTATATAAATTCCAATCTGATCATCAACAAGCTTGC 420
Db 425 |||||CAACTTCCGATCAACAATATTTTATATAAATTCCAATCTGATCATCAACAAGCTTGC 484
Qy 421 |||||CAATGCTTCCATCATCTCTTGGCATGTTTACCTGCGAGTGTGATAGCAGCATTTG 480
Db 485 |||||CAATGCTTCCATCATCTCTTGGCATGTTTACCTGCGAGTGTGATAGCAGCATTTG 544
Qy 481 |||||TCCAATTCATPATGGAACCAAGTATTAAGAAGTTTCCACATTTGTTGATTAAGTGAATGT 540
Db 545 |||||TCCAATTCATPATGGAACCAAGTATTAAGAAGTTTCCACATTTGTTGATTAAGTGAATGT 604
Qy 541 |||||TAACAAGAAAGCAGTTTGGCTTCTCAAGTTTCTTTTGTGCTGACTGCATGCAATTTATA 600
Db 605 |||||TAACAAGAAAGCAGTTTGGCTTCTCAAGTTTCTTTTGTGCTGACTGCATGCAATTTATA 664
Qy 601 |||||GTCTGTCTTAACCCATGAGCGATCTCTACAGATACAGATGCTAACTGGGATATCAAC 660
Db 665 |||||GTCTGTCTTAACCCATGAGCGATCTCTACAGATACAGATGCTAACTGGGATATCAAC 723
Qy 661 |||||AGGTCCAACAAATTAAGAGAG 681
Db 724 |||||AGGTCCAACAAATTAAGAGAG 744
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Job time : 5464.54 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2005, 20:13:31 ; Search time 802.249 Seconds
(without alignments)
9927.475 Million cell updates/sec

Title:	US-10-750-262-1
Perfect score:	1195
Sequence:	1 ccgagactcacggtcaagct.....ggaaaaaaaaaaaaaaaaaa 1195

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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2: geneSeqn1980s:*
3: geneSeqn1990s:*
4: geneSeqn2000s:*
5: geneSeqn2001as:*
6: geneSeqn2002as:*
7: geneSeqn2003as:*
8: geneSeqn2003as:*
9: geneSeqn2003as:*
10: geneSeqn2003cs:*
11: geneSeqn2003as:*
12: geneSeqn2004as:*
13: geneSeqn2004as:*
14: geneSeqn2005as:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1195	100.0	1195	4	AAB93924	AAB93924 P789P full
2	1195	100.0	1195	4	AA664160	AA664160 Human pro
3	1195	100.0	1195	5	ACAA5968	ACAA5968 Prostate
4	1195	100.0	1195	6	AB195531	AB195531 Human P78
5	1195	100.0	1195	6	ABK92128	ABK92128 Prostate
6	1195	100.0	1195	8	ACC95685	ACC95685 Prostate
7	1195	100.0	1195	10	ADB75572	ADB75572 Prostate
8	1195	100.0	1195	10	ADB14328	ADB14328 Human pro
9	1195	100.0	1195	10	AAD63162	AAD63162 Human STEA
10	1195	100.0	1195	10	AAD62763	AAD62763 Human STEA
11	1195	100.0	1195	10	ADG26744	ADG26744 Human pro
12	1195	100.0	1195	11	ADN39612	ADN39612 Cancer/pro
13	1195	100.0	1195	11	ADN39395	ADN39395 Cancer/an
14	1195	100.0	1195	11	ADP88258	ADP88258 Prostate
15	1195	100.0	1195	12	AD106462	AD106462 Human tum
16	1195	100.0	1195	12	AD106436	AD106436 Human tum
17	1195	100.0	1195	12	ADJ75176	ADJ75176 Marker ge
18	1195	100.0	1330	13	ADRI4190	ADRI4190 Human NF-
19	1195	100.0	1330	13	ADU06030	ADU06030 Novel bro

20	1195	100.0	1330	14	ADY15575	Ady15575 DNA	Ady15575 DNA	Ady15575 DNA	Ady15575 DNA
21	1195	100.0	1330	14	ADY19959	Ady19959	Ady19959	Ady19959	Ady19959
22	1193	99.8	1193	3	AAZ49395	AAZ49395	AAZ49395	AAZ49395	AAZ49395
23	1193	99.8	1193	5	AAD07067	AAD07067	AAD07067	AAD07067	AAD07067
24	1193	99.8	1193	14	ADY92658	Ady92658	Ady92658	Ady92658	Ady92658
25	1190	99.6	1294	4	AAK51978	AAK51978	AAK51978	AAK51978	AAK51978
26	1182	98.9	1198	8	ACD02628	ACD02628	ACD02628	ACD02628	ACD02628
27	1181.8	98.9	1193	8	ACD02529	ACD02529	ACD02529	ACD02529	ACD02529
28	1180.4	98.8	1198	8	ACD02629	ACD02629	ACD02629	ACD02629	ACD02629
29	1178	98.6	1277	5	ADL46020	Adl46020	Adl46020	Adl46020	Adl46020
30	1177	98.5	1177	14	ADY73174	Ady73174	Ady73174	Ady73174	Ady73174
31	1177	98.5	1201	13	ADX33625	Adx33625	Adx33625	Adx33625	Adx33625
32	1174.4	98.3	1229	4	AAK52962	AAK52962	AAK52962	AAK52962	AAK52962
33	1166	97.6	1354	12	ADQ22300	Adq22300	Adq22300	Adq22300	Adq22300
34	1048	87.7	1365	8	ACD02599	ACD02599	ACD02599	ACD02599	ACD02599
35	1048	87.7	1365	8	ACD02630	ACD02630	ACD02630	ACD02630	ACD02630
36	1044	87.4	1359	8	ACD02632	ACD02632	ACD02632	ACD02632	ACD02632
37	1042.4	87.2	1369	8	ACD02631	ACD02631	ACD02631	ACD02631	ACD02631
38	827.2	69.2	3627	8	ACD02601	ACD02601	ACD02601	ACD02601	ACD02601
39	825.6	69.1	3627	3	AAZ49396	AAZ49396	AAZ49396	AAZ49396	AAZ49396
40	825.6	69.1	3627	5	AAD07071	AAD07071	AAD07071	AAD07071	AAD07071
41	825.6	69.1	3627	8	ACD02613	ACD02613	ACD02613	ACD02613	ACD02613
42	825.6	69.1	3627	8	ACD02605	ACD02605	ACD02605	ACD02605	ACD02605
43	825.6	69.1	3627	8	ACD02606	ACD02606	ACD02606	ACD02606	ACD02606
44	825.6	69.1	3627	8	ACD02598	ACD02598	ACD02598	ACD02598	ACD02598
45	825.6	69.1	3627	8	ACD02612	ACD02612	ACD02612	ACD02612	ACD02612

ALIGNMENTS

	RESULT 1
ID	AAH93924
XX	AAH93924 standard; cDNA; 1195 BP.
AC	AAH93924;
XX	
DT	04-OCT-2001 (first entry)
XX	
DE	P789P full length cDNA sequence.
XX	
KW	Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis; ss.
OS	Homo sapiens.
XX	
PN	WO200151633-A2.
XX	
PD	19-JUL-2001.
XX	
PF	16-JAN-2001; 2001WO-US001574.
XX	
PR	14-JAN-2000; 2000US-00483672.
XX	
PA	(CORI-) CORIXA CORP.
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG, Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAW; Wang A, Meagher MJ;
XX	
DR	WPI; 2001-425873/45.
PT	New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines.
PS	Claim 1; Page 510; 543pp; English.
CC	The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and

CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnosis and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH9357 to AAH93944 and AAH0115 to AAH01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention
XX

Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1195; DB 4; Length 1195;

Best Local Similarity 100.0%; Pred. No. 4,4e-276;

Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CCGAGACTCAGGCTAAGCTAAGCGGAGAGTGGTGGCTGAAGCCATATATTATATAG 60
DB 1 CCGAGACTCAGGCTAAGCTAAGCGGAGAGTGGTGGCTGAAGCCATATATTATAG 60
QY 61 AATTAAATGAGAAAGCAAGAAAGATCAAAACCAAGAGAACTTTGGAAAATGAGCTTA 120
DB 61 AATTAAATGAGAAAGCAAGAAAGATCAAAACCAAGAGAACTTTGGAAAATGAGCTTA 120
QY 121 GGAAGAAATTTAGAAAGAGAGATTAATTTGCATTAAGACAGGAGAGACGAGATCTTA 180
DB 121 GGAAGAAATTTAGAAAGAGAGATTAATTTGCATTAAGACAGGAGAGACGAGATCTTA 180
QY 181 AAAGACTGCTGCTTTGCAATTTGCACCAACAGCCCATGCTGTAATTTGACGGCTT 240
DB 181 AAAGACTGCTGCTTTGCAATTTGCACCAACAGCCCATGCTGTAATTTGACGGCTT 240
QY 241 CAGAACTTGAAGCAGACAGAGAACTCTTTCCACAGTGGCACTTCCAAATTTAAATAGCTG 300
DB 241 CAGAACTTGAAGCAGACAGAGAACTCTTTCCACAGTGGCACTTCCAAATTTAAATAGCTG 300
QY 301 CATTATATGATCTCTGACTTTTCTTTACCTCTTTCAGAGGAGATTAATCCCTTTAG 360
DB 301 CATTATATGATCTCTGACTTTTCTTTACCTCTTTCAGAGGAGATTAATCCCTTTAG 360
QY 361 CAACCTCCCATCAACAAATATTTTATTAATTCCTGATCCGATCAACCAAGCTCTG 420
DB 361 CAACCTCCCATCAACAAATATTTTATTAATTCCTGATCCGATCAACCAAGCTCTG 420
QY 421 CAATGTTTCCATCACTCTCTTGGCATTTGGTTTACCTGCGAGTGTATAGCAGCAATTG 480
DB 421 CAATGTTTCCATCACTCTCTTGGCATTTGGTTTACCTGCGAGTGTATAGCAGCAATTG 480
QY 481 TCCAACTTCAATATGAGAACCAAGATTAAGAAAGTTTCCACTTTGGTGGATAGTGATG 540
DB 481 TCCAACTTCAATATGAGAACCAAGATTAAGAAAGTTTCCACTTTGGTGGATAGTGATG 540
QY 541 TAACAAGAAAGAGTTGGGCTTCTCAGTTTCTTTTGGCTGACTGATGCAATTTATA 600
DB 541 TAACAAGAAAGAGTTGGGCTTCTCAGTTTCTTTTGGCTGACTGATGCAATTTATA 600
QY 601 GTCGTCTTACCCATGAGCGCATCTCAGATATCAAGTTGCTAACTGGGCATATCAAC 660
DB 601 GTCGTCTTACCCATGAGCGCATCTCAGATATCAAGTTGCTAACTGGGCATATCAAC 660
QY 661 AGGTCCAAAGAAATTAAGAAAGATGCTGATTAAGCATGATGTTTGGAGAAATGAGAAATT 720
DB 661 AGGTCCAAAGAAATTAAGAAAGATGCTGATTAAGCATGATGTTTGGAGAAATGAGAAATT 720
QY 721 ATGTGCTCTGGGAATTTGGGATTTGGCAATACCTGCTGTTGGCTGATCATCTATTTC 780
DB 721 ATGTGCTCTGGGAATTTGGGATTTGGCAATACCTGCTGTTGGCTGATCATCTATTTC 780
QY 781 CATCTGTGAGTGACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGAA 840
DB 781 CATCTGTGAGTGACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGAA 840
QY 841 TTGTTTCCCTTCTACTGGGCAATATCAGCATTTGATTTTGGCTGGAATTAAGTGATAG 900
```

```
DB 841 TTGTTTCCCTTCTACTGGGCAATATCAGCATTTGATTTTGGCAATTAAGTGATAG 900
QY 901 AATTAAGAAATTTGATGATATGATATACCTCCCACTTTATGATGCTGTTTCTTCCAA 960
DB 901 AATTAAGAAATTTGATGATATGATATACCTCCCACTTTATGATGCTGTTTCTTCCAA 960
QY 961 TTGTTTCCCTGATATTTAAAGCATATATTCCTGCGATGCTTGAGAAAGATATCTGA 1020
DB 961 TTGTTTCCCTGATATTTAAAGCATATATTCCTGCGATGCTTGAGAAAGATATCTGA 1020
QY 1021 AGATTGACATGTTGGGAAAGCGTCAACCAAAATTTAAACAACTGATATGTTCCCACT 1080
DB 1021 AGATTGACATGTTGGGAAAGCGTCAACCAAAATTTAAACAACTGATATGTTCCCACT 1080
QY 1081 TGTAGAAATTAAGCTTTTACACATTTTGGTCAATATGATATATTTATCAACCAATT 1140
DB 1081 TGTAGAAATTAAGCTTTTACACATTTTGGTCAATATGATATATTTATCAACCAATT 1140
QY 1141 TCAAGTTTGTATTTGTTAATTAATGATTAATCAAGGAAAAA 1195
DB 1141 TCAAGTTTGTATTTGTTAATTAATGATTAATCAAGGAAAAA 1195
```

RESULT 2

AA64160 standard; cDNA; 1195 BP.

AA64160;

29-JUN-2002 (first entry)

Human prostate cDNA sequence #590.

Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.

Homo sapiens.

WO200173032-A2.

04-OCT-2001.

27-MAR-2001; 2001WO-US009919.

27-MAR-2000; 2000US-00536857.

09-MAY-2000; 2000US-00568100.

12-MAY-2000; 2000US-00570737.

13-JUN-2000; 2000US-00593793.

27-JUN-2000; 2000US-00605783.

09-AUG-2000; 2000US-00636215.

29-AUG-2000; 2000US-00651236.

06-SEP-2000; 2000US-00657279.

02-OCT-2000; 2000US-00679426.

10-OCT-2000; 2000US-00685166.

09-NOV-2000; 2000US-00709729.

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD; Fanger GR, Reltzer MW, Stolk JA, Day CH, Vedvick TS, Carter D; Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA; WPI; 2001-639232/73. P-PSDB; AAU69927.

New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer.

Claim 1, Page 548; 579p; English.

The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and

CC antigen-presenting cells expressing the polypeptides. The antibodies are
 CC useful for detecting the presence of cancer, especially prostate cancer.
 CC The polypeptides, polynucleotides and the antigen-presenting cells are
 CC useful for stimulating and/or expanding T cells specific for a tumour
 CC protein, and for inhibiting the development of cancer especially prostate
 CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
 CC useful for stimulating an immune response, and for treating cancer. The
 CC oligonucleotide is useful for detecting cancer. The present sequence is a
 CC prostate specific polynucleotide of the invention
 XX

Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1195; DB 4; Length 1195;
 Best Local Similarity 100.0%; Pred. No. 4,4e-276;

Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 CCGAGACTCAGCGCTCAAGCTTAAGGCGAAGAGTGGGTGGCTGAACCATCTATTATTATAG 60
Db 1 CCGAGACTCAGCGCTCAAGCTTAAGGCGAAGAGTGGGTGGCTGAACCATCTATTATTATAG 60
Qy 61 AATTATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 61 AATTATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Qy 121 GGAAGAAATTTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 GGAAGAAATTTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Qy 181 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy 241 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 241 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 301 CTATTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 CTATTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 361 CAACTTCCCATCAACATATTTTATTAATTCATTCCTGCTCATCAACAAAGTCTTGC 420
Db 361 CAACTTCCCATCAACATATTTTATTAATTCATTCCTGCTCATCAACAAAGTCTTGC 420
Qy 421 CAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 CAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 481 TCCAACTTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 TCCAACTTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 541 TAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 541 TAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy 601 GTCGCTTCAACCAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GTCGCTTCAACCAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Qy 661 AGGTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 AGGTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy 721 ATGTGCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 721 ATGTGCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy 781 CATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 781 CATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Qy 841 TTGTTCCCTTCTACTGGGCAATACAGCATTTGTTTGGCTGGAAATAGTGATAG 900

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Db 841 TTGTTCCCTTCTACTGGGCAATACAGCATTTGTTTGGCTGGAAATAGTGATAG 900
Qy 901 AATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 AATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Qy 961 TTGTTGCTGATATTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 TTGTTGCTGATATTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy 1021 AGATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1021 AGATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Qy 1081 TGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1081 TGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy 1141 TCAAGTTTGTATTTGTTAATTAATGATTTATTCAGAGAGAGAGAGAGAGAGAGAGAGAG 1195
Db 1141 TCAAGTTTGTATTTGTTAATTAATGATTTATTCAGAGAGAGAGAGAGAGAGAGAGAGAG 1195

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RESULT 3
 ACAS9968
 ID ACAS9968 standard; cDNA; 1195 BP.
 XX
 AC AS9968;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Prostate cancer therapy associated cDNA #655.
 KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KW immunogen; cancer; prostate specific antigen; PSA;
 KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
 KW PMA; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002192763-A1.
 XX
 PD 19-DEC-2002.
 XX
 PF 29-JUN-2001; 2001US-00895793.
 XX
 PR 04-OCT-1999; 99US-0157455P.
 PR 04-OCT-2000; 2000US-00679272.
 PR 28-MAR-2001; 2001US-00822827.
 XX
 (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CARP/) CARTER D.
 PA (LISK/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEL/) SKELLY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOUN/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOYT/) FOY T M.

XX Xu J, Dillon DC, Mutcham JL, Harlocker SL, Jiang Y, Kalos MD,
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D,
PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA, Hural J,
PI McNeill PD, Houghton RL, Y De Basols CV, Foy TM,
XX WPI, 2001-245062/25.
DR P-PSDB; AB071821.
XX Prostate specific protein and its encoding polynucleotide, useful for the
PT treatment and diagnosis of prostate cancer.
XX
PS Example 5, SEQ ID NO 878; 85bp; English.
XX The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This sequence represents a prostate cancer
CC therapy associated cDNA. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?docid=US20020192763
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
Query Match 100.0%; Score 1195; DB 5; Length 1195;
Best Local Similarity 100.0%; Pred. No. 4, 4e-276;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGAGCTCAGCGTCAAGCTAAGCGAGAGTGGGTGGTGAAGCCATATTTATATG 60
DB 1 CCGAGCTCAGCGTCAAGCTAAGCGAGAGTGGGTGGTGAAGCCATATTTATATG 60
QY 61 AATTAATGAAAGCAGAAAAAGCATCAAAACCAGAGAATTGGAAAAATGAAGCTTA 120
DB 61 AATTAATGAAAGCAGAAAAAGCATCAAAACCAGAGAATTGGAAAAATGAAGCTTA 120
QY 121 GGAAGAAATTTAGAAAGACGATTATTGTCATAGACACGAGAGACACGATCTAA 180
DB 121 GGAAGAAATTTAGAAAGACGATTATTGTCATAGACACGAGAGACACGATCTAA 180
QY 181 AAAGACCTGCTTTGTCATTTGACCAAAAGCCCATGTCATGAATTTGATGCCCTT 240
DB 181 AAAGACCTGCTTTGTCATTTGACCAAAAGCCCATGTCATGAATTTGATGCCCTT 240
QY 241 CAGAACTTGACGACACAGAGAACTCTTTCACAGTGGCACTTGCATTTAAATAGCTG 300
DB 241 CAGAACTTGACGACACAGAGAACTCTTTCACAGTGGCACTTGCATTTAAATAGCTG 300
QY 301 CTAATTAATGATCTGACCTTTTCTTTACACTCTTTCAGAGGAAGTAATTCACCTTTAG 360
DB 301 CTAATTAATGATCTGACCTTTTCTTTACACTCTTTCAGAGGAAGTAATTCACCTTTAG 360
QY 361 CAACTCCCATCAACATATTTTATTAATTCATTCCTGGATCAACAAAGTCTTGC 420
DB 361 CAACTCCCATCAACATATTTTATTAATTCATTCCTGGATCAACAAAGTCTTGC 420
QY 421 CAATGTTTCCATCACTCTCTTGGCATTTGTTACCTGCGAGGTGATAGCAGCAATTG 480
DB 421 CAATGTTTCCATCACTCTCTTGGCATTTGTTACCTGCGAGGTGATAGCAGCAATTG 480
QY 481 TCCAACTTCAATATGGAACCAATATAGAAAGTTTCCACTTGGTGAATAGTGAATG 540
DB 481 TCCAACTTCAATATGGAACCAATATAGAAAGTTTCCACTTGGTGAATAGTGAATG 540
QY 541 TAACAAGAAAGAGTTGGGCTCTCAGTTCTTTTGTGTGATGACATGAATTTATA 600
DB 541 TAACAAGAAAGAGTTGGGCTCTCAGTTCTTTTGTGTGATGACATGAATTTATA 600

QY 601 GTCGTCTTACCCAAATGAGCGCATCTCAAGATACAAAGTGTCTAACTGGGCATATCAAC 660
DB 601 GTCGTCTTACCCAAATGAGCGCATCTCAAGATACAAAGTGTCTAACTGGGCATATCAAC 660
QY 661 AGGTCCAAATAAATAAGAAAGATGCTGATTTGACATATATGTTTGGAAATGAGATTT 720
DB 661 AGGTCCAAATAAATAAGAAAGATGCTGATTTGACATATATGTTTGGAAATGAGATTT 720
QY 721 ATGTGCTCTGGGAAATTTGGAGATTTGGCAATATCTGGCTGTGTGGCTGACATCTATTC 780
DB 721 ATGTGCTCTGGGAAATTTGGAGATTTGGCAATATCTGGCTGTGTGGCTGACATCTATTC 780
QY 781 CATCTGTAGTACTCTTTTACATGAGAGAAATTTCACTATATTCAGACCAAGCTAGAA 840
DB 781 CATCTGTAGTACTCTTTTACATGAGAGAAATTTCACTATATTCAGACCAAGCTAGAA 840
QY 841 TTGTTTCCCTTTCTACTGCGGCAATATACAGCATTTGTTTCCCTGGAAATAGTGAATG 900
DB 841 TTGTTTCCCTTTCTACTGCGGCAATATACAGCATTTGTTTCCCTGGAAATAGTGAATG 900
QY 901 ATATAAAACAATTTGATATGATATACACCTCCAACTTTATGATGCTGTTTCTTCCA 960
DB 901 ATATAAAACAATTTGATATGATATACACCTCCAACTTTATGATGCTGTTTCTTCCA 960
QY 961 TTGTTGCTCTGATATTTTAAAGCATATCTATTCCTGCATGCTTGAAGAAAGATATCTGA 1020
DB 961 TTGTTGCTCTGATATTTTAAAGCATATCTATTCCTGCATGCTTGAAGAAAGATATCTGA 1020
QY 1021 AAGATTAGACATGTTGGGAAAGCGTCACCAAAATTAACAAACATGATGTTCCCGT 1080
DB 1021 AAGATTAGACATGTTGGGAAAGCGTCACCAAAATTAACAAACATGATGTTCCCGT 1080
QY 1081 TGTAGAAATTAAGTTTACACACATTTTGTCAATATGATATTTTATATCCAAACAT 1140
DB 1081 TGTAGAAATTAAGTTTACACACATTTTGTCAATATGATATTTTATATCCAAACAT 1140
QY 1141 TCAAGTTGTATTTGTTAATAAATGATTTTCAAGAAAAAATTTTTTTTTT 1195
DB 1141 TCAAGTTGTATTTGTTAATAAATGATTTTCAAGAAAAAATTTTTTTTTT 1195
RESULT 4
ABL95531
ID ABL95531 standard; cDNA; 1195 BP.
XX
AC ABL95531;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P789P cDNA sequence SEQ ID NO 878.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US200202248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-00759143.
XX
PR 25-FEB-1997; 97US-00806099.
XX
PR 01-AUG-1997; 97US-00904804.
XX
PR 10-FEB-1998; 98US-00020956.
XX
PR 25-FEB-1998; 98US-00030607.
XX
PR 14-JUL-1998; 98US-0015453.
XX
PR 23-SEP-1998; 98US-00159812.
XX
PR 15-JAN-1999; 99US-00232149.
XX
PR 09-APR-1999; 99US-00288946.
XX
PR 13-JUL-1999; 99US-00352616.
XX
PR 12-NOV-1999; 99US-00439313.

PR 18-NOV-1999; 99US-00443686.
 PR 14-JAN-2000; 2000US-00483672.
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00568100.
 PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605783.
 PR 10-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 02-OCT-2000; 2000US-00679426.
 PR 10-OCT-2000; 2000US-00685166.
 XX
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIANG/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D,
 PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;
 XX
 DR MPI, 2002-255649/30.
 XX
 PT New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer.
 XX
 PS Claim 1, SEQ ID NO 878; 87bp; English.
 XX
 CC The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a cDNA
 CC described in the invention
 XX
 SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1195; DB 6; Length 1195;
 Best Local Similarity 100.0%; Pred. No. 4,4e-276;
 Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 CTATTATAGATCTGACTTTTCTTTACACTCTTCGAGGGAAGTAATCACCCCTTAG 360
 DB 301 CTATTATAGATCTGACTTTTCTTTACACTCTTCGAGGGAAGTAATCACCCCTTAG 360
 QY 361 CAACCTCCATCAACAATATTTTATTAATAATTCGAATCTGTCATCAACAAAGTCTTG 420
 DB 361 CAACCTCCATCAACAATATTTTATTAATAATTCGAATCTGTCATCAACAAAGTCTTG 420
 QY 421 CAATGTTTCCATCACTCTCTTGCGATGTTTACCTGCGAGGTGATAGCAAGCAATTG 480
 DB 421 CAATGTTTCCATCACTCTCTTGCGATGTTTACCTGCGAGGTGATAGCAAGCAATTG 480
 QY 481 TCCAACTCATATAGAACCAAGTATTAAGAAAGTTCCACATTTGTTGATTAAGTGGATG 540
 DB 481 TCCAACTCATATAGAACCAAGTATTAAGAAAGTTCCACATTTGTTGATTAAGTGGATG 540
 QY 541 TAAAGAAAGAGATTGGAGCTTCTCAGTTTCTTTTTCCTGTAATGCAATTTATA 600
 DB 541 TAAAGAAAGAGATTGGAGCTTCTCAGTTTCTTTTTCCTGTAATGCAATTTATA 600
 QY 601 GTCTGTCTTACCAATGAGGCGATCTCTACAGATACAAAGTTGCTTAACTGGCATATCAAC 660
 DB 601 GTCTGTCTTACCAATGAGGCGATCTCTACAGATACAAAGTTGCTTAACTGGCATATCAAC 660
 QY 661 AGGTCCAAAGAAATTAAGAAAGATGCTGGATTGAGCATGATGTTTGGAAATGAGATTT 720
 DB 661 AGGTCCAAAGAAATTAAGAAAGATGCTGGATTGAGCATGATGTTTGGAAATGAGATTT 720
 QY 721 ATGTGTCTGTGGAAATGTGGATTTGGCAATACCTGCTGTGCTGTGATCTATATTC 780
 DB 721 ATGTGTCTGTGGAAATGTGGATTTGGCAATACCTGCTGTGCTGTGATCTATATTC 780
 QY 781 CATCTGTGATGATCTTTGATGATGAGAGAAATTTTCACTATTTGACAGCAAGCTAGGAA 840
 DB 781 CATCTGTGATGATCTTTGATGATGAGAGAAATTTTCACTATTTGACAGCAAGCTAGGAA 840
 QY 841 TTGTTTCCCTTCTACCTGAGCAATACACGATTAATTTTCTGTAATTAAGTGGATAG 900
 DB 841 TTGTTTCCCTTCTACCTGAGCAATACACGATTAATTTTCTGTAATTAAGTGGATAG 900
 QY 901 ATATATAAACAATTTGATGATGATATACACCTCCAACTTTATGATGCTGTTTCTTCCAA 960
 DB 901 ATATATAAACAATTTGATGATGATATACACCTCCAACTTTATGATGCTGTTTCTTCCAA 960
 QY 961 TTGTTGCTGTATTTTAAAGCATATCTTCTGCAATGCTTGAAGAAAGATATCTTA 1020
 DB 961 TTGTTGCTGTATTTTAAAGCATATCTTCTGCAATGCTTGAAGAAAGATATCTTA 1020
 QY 1021 AGATTAGACATGTTGGGAAGAGCTCACCAAAATTAACAAACCTGATATGTTCCCACT 1080
 DB 1021 AGATTAGACATGTTGGGAAGAGCTCACCAAAATTAACAAACCTGATATGTTCCCACT 1080
 QY 1081 TGTAGAAATTAATCTTTTACACACATTTTGTTCATATGATATATTTATATACCAACAT 1140
 DB 1081 TGTAGAAATTAATCTTTTACACACATTTTGTTCATATGATATATTTATATACCAACAT 1140
 QY 1141 TCAAGTTGTATTTGTTATTAATAATGATTTATCAAGAAAAAATTTTTTTTTT 1195
 DB 1141 TCAAGTTGTATTTGTTATTAATAATGATTTATCAAGAAAAAATTTTTTTTTT 1195
 RESULT 5
 ABR92128
 ID ABR92128 standard; DNA; 1195 BP.
 XX
 AC ABR92128;
 XX
 DT 15-AUG-2002 (first entry)
 XX
 DE Prostate cancer-associated DNA sequence #14.
 XX
 KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;

KM gene therapy; gene; ds.
 XX Mammalia.
 OS
 PN WO200230268-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US032045.
 XX
 PR 13-OCT-2000; 2000US-00687576.
 PR 08-DEC-2000; 2000US-00733288.
 PR 08-DEC-2000; 2000US-00733742.
 PR 24-JAN-2001; 2001US-0263957P.
 PR 16-MAR-2001; 2001US-0276791P.
 PR 16-MAR-2001; 2001US-0276888P.
 PR 06-APR-2001; 2001US-0281922P.
 PR 24-APR-2001; 2001US-0286214P.
 PR 30-APR-2001; 2001US-00847046.
 PR 04-MAY-2001; 2001US-0288589P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
 XX
 DR WPI; 2002-471335/50.
 DR P-8SDB; ABG61813.
 XX
 PT Detecting a prostate cancer-associated transcript in a cell in a patient,
 PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
 PT by determining if prostate cancer-associated genes are expressed in a
 PT prostate tissue.
 XX
 PS Claim 22; Page 311-312; 436pp; English.
 XX
 CC The present invention relates to methods of detecting a prostate cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with prostate cancer-
 CC associated polynucleotides (designated PC genes) that selectively
 CC hybridize to a sequence that is at least 80% identical to them. The
 CC prostate cancer-associated polynucleotide sequences are differentially
 CC expressed in prostate tumour tissue or in prostate cancer and are derived
 CC from the tissues of various organisms such as humans or other mammals
 CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
 CC associated genes are useful for diagnosing or treating prostate cancer,
 CC as well as for identifying modulators of prostate cancer or agents that
 CC inhibit prostate cancer. The nucleic acid sequences are particularly
 CC useful in gene therapy, as a vaccine or in antisense applications.
 CC ABK32115-ABK92263 represent prostate cancer-associated polynucleotide
 CC sequences
 XX
 SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 1195; DB 6; Length 1195;
 Best Local Similarity 100.0%; Pred. No. 4,4e-276;
 Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGAGACTCAGCGTCAAGCTAAGCGGAAGTGGGTGCTGAAGCCATATCTATTTATG 60
 DB 1 CCGAGACTCAGCGTCAAGCTAAGCGGAAGTGGGTGCTGAAGCCATATCTATTTATG 60
 QY 61 AATTATGGAAGCAGAAAAGACATCAAAACCAAGAGAACTTTGAAAATGAAGCCTA 120
 DB 61 AATTATGGAAGCAGAAAAGACATCAAAACCAAGAGAACTTTGAAAATGAAGCCTA 120
 QY 121 GGAGAATTTAGAAAGAGAGATTTATGATTAAGACAGGAGAGAGACCATGCTTA 180
 DB 121 GGAGAATTTAGAAAGAGAGATTTATGATTAAGAGACAGGAGAGAGACCATGCTTA 180
 QY 181 AAAAGCCTGTGCTTTTGCAATTTGCAACCAACAGCCCATGCTGATGATTTGATGCCCTT 240
 DB 181 AAAAGCCTGTGCTTTTGCAATTTGCAACCAACAGCCCATGCTGATGATTTGATGCCCTT 240

QY 241 CAGAACTTCAGACACACAGAGAACTCTTTGCAACAGTGGCACTTGGCAATTTAAATAGCTG 300
 DB 241 CAGAACTTCAGACACACAGAGAACTCTTTGCAACAGTGGCACTTGGCAATTTAAATAGCTG 300
 QY 301 CTATTATAGATCTCTGACTTTTCTTACACTCTTCTGAGGAGATTAATCACCCCTTAG 360
 DB 301 CTATTATAGATCTCTGACTTTTCTTACACTCTTCTGAGGAGATTAATCACCCCTTAG 360
 QY 361 CAATCTCCATCAACAAATATTTTATATAAAATTCGAATCTGGTGCATCAACAAAGCTTTC 420
 DB 361 CAATCTCCATCAACAAATATTTTATATAAAATTCGAATCTGGTGCATCAACAAAGCTTTC 420
 QY 421 CAATGTTTCCATCACTCTCTGGCAATTTGTTTACCTGCCAGGTGATATGACCAATTC 480
 DB 421 CAATGTTTCCATCACTCTCTGGCAATTTGTTTACCTGCCAGGTGATATGACCAATTC 480
 QY 481 TCCAACTTCATATAGAACCAAGATATAAGAGTTTCCACATTTGGTGGATAGTGT 540
 DB 481 TCCAACTTCATATAGAACCAAGATATAAGAGTTTCCACATTTGGTGGATAGTGT 540
 QY 541 TAAAGAAAGACAGTTTGGGCTTCTCAGTTTCTTTTGTCTGTACTGATGCAATTTTA 600
 DB 541 TAAAGAAAGACAGTTTGGGCTTCTCAGTTTCTTTTGTCTGTACTGATGCAATTTTA 600
 QY 601 GTCTGTCTTACCAATGAGCGGATCTTACATATCAAGTTGCTAACTGGGCAATATCAAC 660
 DB 601 GTCTGTCTTACCAATGAGCGGATCTTACATATCAAGTTGCTAACTGGGCAATATCAAC 660
 QY 661 AGGTCCAAACAAATTAAGAGAGTGGCTGGAATTGAGCATGATGTTTGGAGAAATGAGATTT 720
 DB 661 AGGTCCAAACAAATTAAGAGAGTGGCTGGAATTGAGCATGATGTTTGGAGAAATGAGATTT 720
 QY 721 ATGTCTCTCGGAATTTGGGATTTGGCAATATCTGCTCTGTGGCTGTGACATTTATTC 780
 DB 721 ATGTCTCTCGGAATTTGGGATTTGGCAATATCTGCTCTGTGGCTGTGACATTTATTC 780
 QY 781 CATCTGAGAGTACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAA 840
 DB 781 CATCTGAGAGTACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAA 840
 QY 841 TTGTTTCCCTCTACTGGGACCAATACAGCATTTGATTTTGGCTGGAATAGTGGATAG 900
 DB 841 TTGTTTCCCTCTACTGGGACCAATACAGCATTTGATTTTGGCTGGAATAGTGGATAG 900
 QY 901 AATATAAAACAATTTGTATGTATATACACCTCCAACTTTATGATAGCTGTTTCTTCCAA 960
 DB 901 AATATAAAACAATTTGTATGTATATACACCTCCAACTTTATGATAGCTGTTTCTTCCAA 960
 QY 961 TTGTTGCTCTGATATTTTAAAGACATATCTTCCCATGCTTGGAGAAAGATATCTGA 1020
 DB 961 TTGTTGCTCTGATATTTTAAAGACATATCTTCCCATGCTTGGAGAAAGATATCTGA 1020
 QY 1021 AGATTAGACATGTTGGGAAGAGCTCACCAAAATTTAACAAAATGAGATATGTTCCAGT 1080
 DB 1021 AGATTAGACATGTTGGGAAGAGCTCACCAAAATTTAACAAAATGAGATATGTTCCAGT 1080
 QY 1081 TGTAGAAATTAAGTTTACACACATTTTGTTCATATTTGATATTTATATTCACCAATTT 1140
 DB 1081 TGTAGAAATTAAGTTTACACACATTTTGTTCATATTTGATATTTATATTCACCAATTT 1140
 QY 1141 TCAAGTTTGTATTTGTTAATATAAAGATATTTCAAGGAAAAAATTTTTTTTTT 1195
 DB 1141 TCAAGTTTGTATTTGTTAATATAAAGATATTTCAAGGAAAAAATTTTTTTTTT 1195
 RESULT 6
 ACC95695
 ID ACC95695 standard; cDNA; 1195 BP.
 XX
 AC ACC95695;
 XX
 DT 28-AUG-2003 (first entry)

XX Prostate tumour specific cDNA sequence SEQ ID 878.
DE
XX
XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KM Immune response; prostate cancer; ss.
KM
XX Homo sapiens.
XX
XX MO200289747-A2.
XX
XX 14-NOV-2002.
XX
XX 09-MAY-2002; 2002MO-US014753.
XX
XX 09-MAY-2001; 2001US-00852911.
XX 29-JUN-2001; 2001US-00895814.
XX 10-DEC-2001; 2001US-00012896.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kelso MD, Ranger GR, Retter MW, Stolk JA, Day CH, Vedyick TS;
PI Carter D, Li SX, Wang A, Skeiky YAM, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De Baseolac, Foy TM, Watanabe Y;
PI Deng T;
XX
XX WPI; 2003-167130/16.
XX
XX New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
XX Example 5; Page 617-618; 691pp; English.
XX
XX The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
XX Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1195; DB 8; Length 1195;
Best Local Similarity 100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGAGACTCAGCGTCAAGTAAAGCGAAGAGTGGGTGGCTGAAGCCATCTATTTATAG 60
DB 1 CCGAGACTCAGCGTCAAGTAAAGCGAAGAGTGGGTGGCTGAAGCCATCTATTTATAG 60
QY 61 AATTATGGAAGCAGAAAAGACATCAAAACCAAGAACTTTGGAAAATGAGCTTA 120
DB 61 AATTATGGAAGCAGAAAAGACATCAAAACCAAGAACTTTGGAAAATGAGCTTA 120
QY 121 GGAGAAATTTAAGAAAGAGATTTATTTGATTAAGACAGGGAGAGACCGAGCTGTAA 180
DB 121 GGAGAAATTTAAGAAAGAGATTTATTTGATTAAGACAGGGAGAGACCGAGCTGTAA 180
QY 181 AAGAGCTGTCTTTTGGATTTGACACCAACAGCCCATGCTGAATTTGACTGCCCTT 240
DB 181 AAGAGCTGTCTTTTGGATTTGACACCAACAGCCCATGCTGAATTTGACTGCCCTT 240
QY 241 CAGAACTTCAGCAGACAGAGAACTTTTTCACAGTGGCCTTGGCAATTTAAATAGCTG 300
DB 241 CAGAACTTCAGCAGACAGAGAACTTTTTCACAGTGGCCTTGGCAATTTAAATAGCTG 300
QY 301 CTATTATAGCATCTGACTCTTTCTTTACACTCTTCTGAGGAGAGTAATCACCCCTTAG 360
DB 301 CTATTATAGCATCTGACTCTTTCTTTACACTCTTCTGAGGAGAGTAATCACCCCTTAG 360
QY 361 CAATTCCTCATCAACATATTTTATTAATTCATCTGTCTATCAACAAAGCTTTCG 420

DB 361 CAATTCCTCATCAACATATTTTATTAATTCATCTGTCTATCAACAAAGCTTTCG 420
QY 421 CAATGTTTCCATCACTCTCTTGGCAATGGTTTACCTGCCAGGATGATGAGCAATTCG 480
DB 421 CAATGTTTCCATCACTCTCTTGGCAATGGTTTACCTGCCAGGATGATGAGCAATTCG 480
QY 481 TCCAACTTCATTAATGGAACCAATATAGAAAGTTTCCATCTGATGATGATGATGATG 540
DB 481 TCCAACTTCATTAATGGAACCAATATAGAAAGTTTCCATCTGATGATGATGATGATG 540
QY 541 TAAAGAAAGAGAGTTTGGCTTCTCACTTTCTTTTGGCTGATGATGATGATGATGATG 600
DB 541 TAAAGAAAGAGAGTTTGGCTTCTCACTTTCTTTTGGCTGATGATGATGATGATGATG 600
QY 601 GTCTGCTTACCAATGAGGCGATCTCAAGATACAAAGTTGTAACCTGGGCAATTCAC 660
DB 601 GTCTGCTTACCAATGAGGCGATCTCAAGATACAAAGTTGTAACCTGGGCAATTCAC 660
QY 661 AGGTCCACAAATTAAGAGATGCTGATGATGATGATGATGATGATGATGATGATGATG 720
DB 661 AGGTCCACAAATTAAGAGATGCTGATGATGATGATGATGATGATGATGATGATGATG 720
QY 721 ATGTCTCTGGAATTTGGGATTTGGCAATGATGATGATGATGATGATGATGATGATGATG 780
DB 721 ATGTCTCTGGAATTTGGGATTTGGCAATGATGATGATGATGATGATGATGATGATGATG 780
QY 781 CATCTGAGTGACTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
DB 781 CATCTGAGTGACTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 841 TTGTTTCCCTTCTACTGCGGACAAATACAGCATTTGTTTGGCTGGAATTAAGTGAATG 900
DB 841 TTGTTTCCCTTCTACTGCGGACAAATACAGCATTTGTTTGGCTGGAATTAAGTGAATG 900
QY 901 ATATTAACAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
DB 901 ATATTAACAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
QY 961 TTGTTTCCCTTCTACTGCGGACAAATACAGCATTTGTTTGGCTGGAATTAAGTGAATG 1020
DB 961 TTGTTTCCCTTCTACTGCGGACAAATACAGCATTTGTTTGGCTGGAATTAAGTGAATG 1020
QY 1021 AGATTAGCATGTTTGGGAAAGAGTCAACCAAAATTAACAAACCTGATGATGATGATG 1080
DB 1021 AGATTAGCATGTTTGGGAAAGAGTCAACCAAAATTAACAAACCTGATGATGATGATG 1080
QY 1081 TGTAGAAATTAAGTGTATTAACCAATTTTGTCAATATGATATTTTATCACCAACATT 1140
DB 1141 TGTAGAAATTAAGTGTATTAACCAATTTTGTCAATATGATATTTTATCACCAACATT 1140
QY 1141 TCAAGTTTGTATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1195
DB 1141 TCAAGTTTGTATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1195
RESULT 7
ADB75572
ID ADB75572 standard; cDNA; 1195 BP.
XX
XX ADB75572;
AC
XX
XX 04-DEC-2003 (first entry)
DT
XX
XX Prostate cancer marker cDNA.
DE
XX
XX Prostate; cancer; cytostatic; gene therapy; marker; ss.
KM
XX
XX Homo sapiens.
OS
XX
XX MO2003009814-A2.
PN
XX
XX 06-FEB-2003.
PD

XX 25-JUL-2002; 2002WO-US023913.
PF
XX
XX 25-JUL-2001; 2001US-0307982P.
PR 22-AUG-2001; 2001US-0314356P.
PR 25-SEP-2001; 2001US-0325020P.
PR 12-DEC-2001; 2001US-0341746P.
PR 05-MAR-2002; 2002US-0362158P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
PI Hoersht S, Kamatkar S, Womsey AM, Glatk K, Zhao X, Anderson D;
XX
XX WPI; 2003-248033/24.
XX
XX New nucleic acid molecule, useful for diagnosing or treating prostate
PT cancer.
XX
XX
XX Disclosure; SEQ ID NO 396; 99pp; English.
XX
XX The invention relates to newly discovered cancer markers associated with
CC the cancerous state of prostate cells. Also disclosed is a method of
CC assessing whether a patient is afflicted with prostate cancer. The method
CC of the invention involves assessing whether a patient is afflicted with
CC prostate cancer by comparing the level of expression of a marker in a
CC patient sample and the normal level of expression of the marker in a
CC control non-prostate cancer sample, where a significant increase in the
CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC AD875177-AD875631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1195; DB 10; Length 1195;
Best Local Similarity 100.0%; Pred. No. 4,4e-276;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGAGACTCAGCGTCAAGCTTAAGGCGAAGAGTGGTGGCTGAAGCCATATTTATAG 60
DB 1 CCGAGCTCAGCGTCAAGCTTAAGGCGAAGAGTGGTGGCTGAAGCCATATTTATAG 60
QY 61 AATTAATGAGAAAGCAGAAAGACATCAAAACCAAGAACTTTGAAATGACCTTA 120
DB 61 AATTAATGAGAAAGCAGAAAGACATCAAAACCAAGAACTTTGAAATGACCTTA 120
QY 121 GGAGAAATTTAGAGAGAGATTTGATTAAGGACGCGGAGAGACAGCATGCTAA 180
DB 121 GGAGAAATTTAGAGAGAGATTTGATTAAGGACGCGGAGAGACAGCATGCTAA 180
QY 181 AAAAGACTGTGCTTTTGAATTTGACCAAAACAGCCCATGCTGATTTGACTGCCCTT 240
DB 181 AAAAGACTGTGCTTTTGAATTTGACCAAAACAGCCCATGCTGATTTGACTGCCCTT 240
QY 241 CAGAACTTACGACACACAGAACTTTTTCACAGTGGGCACTTCCAAATTAATATGCTG 300
DB 241 CAGAACTTACGACACACAGAACTTTTTCACAGTGGGCACTTCCAAATTAATATGCTG 300
QY 301 CATATTATACATCTGACTTTCTTTTACCTTCTGAGGGAGATTAATCACTTTAG 360
DB 301 CATATTATACATCTGACTTTCTTTTACCTTCTGAGGGAGATTAATCACTTTAG 360
QY 361 CAACTTCCATCAACATATTTTATTAATTTCCATTCCTGATCAACAAAGTCTTG 420
DB 361 CAACTTCCATCAACATATTTTATTAATTTCCATTCCTGATCAACAAAGTCTTG 420
QY 421 CAATGTTTCATCACTCTTCTGCAATGGTTTACCTGCGAGTGTGATGACGCAATTG 480
DB 421 CAATGTTTCATCACTCTTCTGCAATGGTTTACCTGCGAGTGTGATGACGCAATTG 480

DB 421 CAATGTTTCATCACTCTTCTGCAATGGTTTACCTGCGAGTGTGATGACGCAATTG 480
QY 481 TCCAACTTCAATATGAAACCAAGTAAAGATTTCACATTTGTTGATAAGTATGT 540
DB 481 TCCAACTTCAATATGAAACCAAGTAAAGATTTCACATTTGTTGATAAGTATGT 540
QY 541 TAAACAAGAAAGAGTTTGGGCTTCTCAAGTTCTTTTGTGCTGATGATGAAATTTATA 600
DB 541 TAAACAAGAAAGAGTTTGGGCTTCTCAAGTTCTTTTGTGCTGATGATGAAATTTATA 600
QY 601 GTCTGCTTACCAATGAGGCGATCTTCAAGTACAGATCAAGTTGCTAAATGGGATTCAC 660
DB 601 GTCTGCTTACCAATGAGGCGATCTTCAAGTACAGATCAAGTTGCTAAATGGGATTCAC 660
QY 661 AGGTCCAAACAAATTAAGAGATGCTGATTTGACATGATGTTTGAATGAGATT 720
DB 661 AGGTCCAAACAAATTAAGAGATGCTGATTTGACATGATGTTTGAATGAGATT 720
QY 721 ATGTGCTCTGGGAATTTGGGATTTGCAATACCTGCTGTTGGCTGATCATCTATTC 780
DB 721 ATGTGCTCTGGGAATTTGGGATTTGCAATACCTGCTGTTGGCTGATCATCTATTC 780
QY 781 CATCTGATGATGATCTTTGACATGAGAGATTTCACTATTTCAAGCAAGCTAGGAA 840
DB 781 CATCTGATGATGATCTTTGACATGAGAGATTTCACTATTTCAAGCAAGCTAGGAA 840
QY 841 TTGTTTCCCTTCTACTGGGCAACATACACGATTTGATTTGCTGGAATGATGATG 900
DB 841 TTGTTTCCCTTCTACTGGGCAACATACACGATTTGATTTGCTGGAATGATGATG 900
QY 901 ATATTAACAAATTTGATGATGATATACACCTCCAACTTTATGATGATGATGATG 960
DB 901 ATATTAACAAATTTGATGATGATATACACCTCCAACTTTATGATGATGATGATG 960
QY 961 TTGTTGCTGCTGATTTTAAAGACATGATTTCTGCTGATGATGATGATGATGATG 1020
DB 961 TTGTTGCTGCTGATTTTAAAGACATGATTTCTGCTGATGATGATGATGATGATG 1020
QY 1021 AGATTAGACATGTTGGAGAGACGTACCAAAATTTAACAAAATGATGATGATGATG 1080
DB 1021 AGATTAGACATGTTGGAGAGACGTACCAAAATTTAACAAAATGATGATGATGATG 1080
QY 1081 TGTAGAAATTAATCTGTTTACACACATTTTGTTCAAATTTGATTTATTTATCA 1140
DB 1081 TGTAGAAATTAATCTGTTTACACACATTTTGTTCAAATTTGATTTATTTATCA 1140
QY 1141 TCAAGTTTGTATTTGATTAATTAATGATTTATCAAGAAAAA 1195
DB 1141 TCAAGTTTGTATTTGATTAATTAATGATTTATCAAGAAAAA 1195
RESULT 8
ADBI4328
ID ADBI4328 standard; cDNA; 1195 BP.
XX
XX ADBI4328;
XX
XX 18-DEC-2003 (first entry)
XX
XX
DE Human prostate specific full length cDNA P789P.
XX
XX Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
XX gene therapy; cell therapy; vaccine; T-cell epitope;
XX class I major histocompatibility complex allele; HMC; prostate cancer;
XX tumour; antigen presenting cell.
OS Homo sapiens.
XX
XX US2003185830-A1.
XX
XX 02-OCT-2003.
XX
XX 12-NOV-2002; 2002US-00294025.
PF


```
OY 901 ATATATAAACTTTGTATGTATATACACTCCAACTTTTATGATAGCTGTTCCTTCGA 960
DB 901 ATATATAAACTTTGTATGTATATACACTCCAACTTTTATGATAGCTGTTCCTTCGA 960
OY 961 TTGTTGTCCTGATTTTAAAGCACTATTTCTGCGCATGCTTGAGGAAGAATATCTGA 1020
DB 961 TTGTTGTCCTGATTTTAAAGCACTATTTCTGCGCATGCTTGAGGAAGAATATCTGA 1020
OY 1021 AGATTAGACATGTTGGGAAGCGTCACCAAAATTACAAACTGAGATATGTTCCCACT 1080
DB 1021 AGATTAGACATGTTGGGAAGCGTCACCAAAATTACAAACTGAGATATGTTCCCACT 1080
OY 1081 TGTAGAAATTACTGTTTACACACATTTTGTTCATATTTGATATATTTTATCCAACTT 1140
DB 1081 TGTAGAAATTACTGTTTACACACATTTTGTTCATATTTGATATATTTTATCCAACTT 1140
OY 1141 TCAAGTTGTATTTGTTAATAAATGATTTTCAAGGAAAAAATTTTAAAAA 1195
DB 1141 TCAAGTTGTATTTGTTAATAAATGATTTTCAAGGAAAAAATTTTAAAAA 1195

RESULT 9
AAd63162
ID AAd63162 standard; DNA; 1195 BP.
AC AAd63162;
XX 12-FEB-2004 (first entry)
DE Human STEAP (six transmembrane epithelial antigen of the prostate) DNA.
XX Human; breast cancer; metastasis; differential modulation; therapy;
XX STEAP; six transmembrane epithelial antigen of the prostate; ds.
XX Homo sapiens.
XX US2003190656-A1.
XX 09-OCT-2003.
XX 21-MAR-2003; 2003US-00393590.
XX 29-MAR-2002; 2002US-0368789P.
XX (WANG/) WANG Y.
XX Wang Y;
XX WPI; 2003-831621/77.
XX Prognosticating metastasis in a breast cancer patient comprises
XX identifying differential modulation of each gene relative to the
XX expression of the same genes in a normal population in combination of
XX genes.
XX Example 2; Page 54-55; Ovp; English.
XX The present invention relates to a method of prognosticating metastasis
XX in a breast cancer patient involves identifying differential modulation
XX of each gene relative to the expression of the same genes in a normal
XX population in combination of genes. The invention is useful for
XX prognosticating breast cancer in a patient. The present sequence is human
XX STEAP (six transmembrane epithelial antigen of the prostate) DNA used to
XX illustrate the method of the invention.
XX Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 1195; DB 10; Length 1195;
XX Best Local Similarity 100.0%; Pred. No. 4.4e-276;
XX Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCGAGACTCAGCGTCAAGCTAAGGCGAAGGTGGGTGGCTGAAGCCATCTACTATTATATAG 60
```

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DB 1 CCGAGACTCAGCGTCAAGCTAAGGCGAAGGTGGGTGGCTGAAGCCATCTACTATTATATAG 60
OY 61 AATTATGAAAAAGCAAAAAACATCACAAAACAAAGAAACCTTGGAAAAATGAAGCTTA 120
DB 61 AATTATGAAAAAGCAAAAAACATCACAAAACAAAGAAACCTTGGAAAAATGAAGCTTA 120
OY 121 GGAAGAAATTTGAAAGAAAGCATTTATTTGCTAAGGACAGGGGAGACCCAGCATGTGCTAA 180
DB 121 GGAAGAAATTTGAAAGAAAGCATTTATTTGCTAAGGACAGGGGAGACCCAGCATGTGCTAA 180
OY 181 AAAGACCTGTCTTTTGGCATTTGGACCAAAACAGCCCAATGCTGATGAATTTTGAATGCTTTC 240
DB 181 AAAGACCTGTCTTTTGGCATTTGGACCAAAACAGCCCAATGCTGATGAATTTTGAATGCTTTC 240
OY 241 CAGAACTTCAGCACACACAGAACTTTTCCACAGTGGCATTTGCCAATTTAAATATAGTGTG 300
DB 241 CAGAACTTCAGCACACACAGAACTTTTCCACAGTGGCATTTGCCAATTTAAATATAGTGTG 300
OY 301 CTATTATATGACATCTCTGACCTTTTCTTTTACACTCTCTGAGGGAAGTAAATTCACCTTTAG 360
DB 301 CTATTATATGACATCTCTGACCTTTTCTTTTACACTCTCTGAGGGAAGTAAATTCACCTTTAG 360
OY 361 CAACTTCCCATCAACAATATTTTATAAAATTCGAATCTGTGATCAACAAAGTCTTGC 420
DB 361 CAACTTCCCATCAACAATATTTTATAAAATTCGAATCTGTGATCAACAAAGTCTTGC 420
OY 421 CAATGTTTCCATCATCTCTCTTGGCAGTGTGTTTACCTGCCAGTGTGATATACAGCAATTTG 480
DB 421 CAATGTTTCCATCATCTCTCTTGGCAGTGTGTTTACCTGCCAGTGTGATATACAGCAATTTG 480
OY 481 TCCAACTTCATATGGAACCAAGTATTAAGAGTTTCCACATTTGGTGTGATTAAGTGAATGT 540
DB 481 TCCAACTTCATATGGAACCAAGTATTAAGAGTTTCCACATTTGGTGTGATTAAGTGAATGT 540
OY 541 TTAACAAGAAAGCAGTTTGGGCTTCTCACTTTCTTTTGTCTGTATCTGCATSCAATTTTAA 600
DB 541 TTAACAAGAAAGCAGTTTGGGCTTCTCACTTTCTTTTGTCTGTATCTGCATSCAATTTTAA 600
OY 601 GTCTGTCTTACCCAATGAGGCGATCTTACAGATACCAATGTTGCTAACTGGCATATCAAC 660
DB 601 GTCTGTCTTACCCAATGAGGCGATCTTACAGATACCAATGTTGCTAACTGGCATATCAAC 660
OY 661 AGGTCCAAACAAATTAAGAATGCTGATTTGAGCATGATGTTGGAATGAGATTT 720
DB 661 AGGTCCAAACAAATTAAGAATGCTGATTTGAGCATGATGTTGGAATGAGATTT 720
OY 721 ATGTGCTCTGGAATTTGGGATTTGGCAATACCTGCTGTGTGCTGTGACATCTATTC 780
DB 721 ATGTGCTCTGGAATTTGGGATTTGGCAATACCTGCTGTGTGCTGTGACATCTATTC 780
OY 781 CATCTGTAGTACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTTAGGA 840
DB 781 CATCTGTAGTACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTTAGGA 840
OY 841 TTGTTTCCCTTACTGCGGCAATAACGCAATGATTTTTCCTGGAATAAGTGAATG 900
DB 841 TTGTTTCCCTTACTGCGGCAATAACGCAATGATTTTTCCTGGAATAAGTGAATG 900
OY 901 ATATATAAACTTTGTATGTATATACACTCCAACTTTTATGATAGCTGTTCCTTCGA 960
DB 901 ATATATAAACTTTGTATGTATATACACTCCAACTTTTATGATAGCTGTTCCTTCGA 960
OY 961 TTGTTGTCCTGATTTTAAAGCACTATTTCTGCGCATGCTTGAGGAAGAATATCTGA 1020
DB 961 TTGTTGTCCTGATTTTAAAGCACTATTTCTGCGCATGCTTGAGGAAGAATATCTGA 1020
OY 1021 AGATTAGACATGTTGGGAAGCGTCACCAAAATTACAAACTGAGATATGTTCCCACT 1080
DB 1021 AGATTAGACATGTTGGGAAGCGTCACCAAAATTACAAACTGAGATATGTTCCCACT 1080
OY 1081 TGTAGAAATTACTGTTTACACACATTTTGTTCATATTTGATATATTTTATCCAACTT 1140
DB 1081 TGTAGAAATTACTGTTTACACACATTTTGTTCATATTTGATATATTTTATCCAACTT 1140
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Db 1081 TGTAGAACTTACTGTTTACACACATTTTGTTCATATTTGATATATTTTATTCACCAACATTT 1140
Oy 1141 TCAAGTTTGTATTTGTTAATAAATGATTATTCAGGAAAAAATTTTTTTT 1195
Db 1141 TCAAGTTTGTATTTGTTAATAAATGATTATTCAGGAAAAAATTTTTTTT 1195

RESULT 10
AAD62763 ID AAD62763 standard; DNA; 1195 BP.
AC AAD62763;
DT 12-FEB-2004 (first entry)
DE Human STEAP (six transmembrane epithelial antigen of the prostate) DNA.
XX
XX Human; cancer; differential modulation; gene expression profile; STEAP;
XX six transmembrane epithelial antigen of the prostate; ds.
XX
OS Homo sapiens.
XX
XX US2003194733-A1.
XX
XX 16-OCT-2003.
XX
XX 21-MAR-2003; 2003US-00393567.
XX
XX 29-MAR-2002; 2002US-0368667P.
XX
XX (WANG/) WANG Y.
XX
XX Wang Y;
XX
XX WPI; 2003-844450/78.
XX
XX
XX Diagnosing cancer comprises identifying differential modulation of each
XX PT gene (relative to the expression of the same genes in a normal
XX PT population) in a combination of genes.
XX
XX
XX Claim 4; Page 54-55; Opp; English.
XX
XX The invention relates to a method for diagnosing cancer. The method
XX CC comprising identifying differential modulation of each gene (relative to
XX CC the expression of the same genes in a normal population) in a combination
XX CC of genes. The method, diagnostic portfolio and the kit are useful in
XX CC diagnosing cancer. The method may also be used for determining gene
XX CC expression profiles. The present sequence is human STEAP (six
XX CC transmembrane epithelial antigen of the prostate) DNA used to illustrate
XX CC the method of the invention
XX
XX
XX Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 1195; DB 10; Length 1195;
XX Best Local Similarity 100.0%; Pred. No. 4, 4e-276;
XX Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGAGAGCTACCGGTCAAGCTAAGCGGAAGTGGTGGCTGAAGCCATTAATTTATAG 60
Db 1 CGAGAGCTACCGGTCAAGCTAAGCGGAAGTGGTGGCTGAAGCCATTAATTTATAG 60
Oy 61 AATTAATGGAAGCAGAAAAAGATCAAAACCAAGAAAGCTTTGGAAAAATGAAGCTTA 120
Db 61 AATTAATGGAAGCAGAAAAAGATCAAAACCAAGAAAGCTTTGGAAAAATGAAGCTTA 120
Oy 121 GGAAGAAATTTTGAAGAAAGAGATTAATTTGATTAAGACACGGAGAGAGACCATGCTTA 180
Db 121 GGAAGAAATTTTGAAGAAAGAGATTAATTTGATTAAGACACGGAGAGAGACCATGCTTA 180
Oy 181 AAGAGACTGTGCTTTTGACATTTTGACCAAAACAGCCCATGCTGAATTTGACTGCCCTT 240
Db 181 AAGAGACTGTGCTTTTGACATTTTGACCAAAACAGCCCATGCTGAATTTGACTGCCCTT 240
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Oy 241 CAGAACTTCAGCACACACAGAAACTCTTTCACAGTGGCACTTCCAAATTAATATAGCTG 300
Db 241 CAGAACTTCAGCACACACAGAAACTCTTTCACAGTGGCACTTCCAAATTAATATAGCTG 300
Oy 301 CTATTAATGACATCTGACCTTTTCTTTACACTCTTTCAGGGAAGTAATTCACCTTTAG 360
Db 301 CTATTAATGACATCTGACCTTTTCTTTACACTCTTTCAGGGAAGTAATTCACCTTTAG 360
Oy 361 CAATCCCATCAACAATATTTTATTAATTTCCATCCCTGATCAACAAGCTCTGC 420
Db 361 CAATCCCATCAACAATATTTTATTAATTTCCATCCCTGATCAACAAGCTCTGC 420
Oy 421 CAATGTTTCCATCACTCTCTTGGCAATGGTTTACCTGCGCAGGTGTGATAGCAATTTG 480
Db 421 CAATGTTTCCATCACTCTCTTGGCAATGGTTTACCTGCGCAGGTGTGATAGCAATTTG 480
Oy 481 TCCAACTTCATTAATGGAACCAAGTATTAAGAGTTTCCAACTGTTGATTAAGTGAATGT 540
Db 481 TCCAACTTCATTAATGGAACCAAGTATTAAGAGTTTCCAACTGTTGATTAAGTGAATGT 540
Oy 541 TAACAGAAAGCAGTTTGGCTTCTGAGTTTCTTTTGTCTGATCTGCAATTTATA 600
Db 541 TAACAGAAAGCAGTTTGGCTTCTGAGTTTCTTTTGTCTGATCTGCAATTTATA 600
Oy 601 GTCTGCTTAACCCCAATGAGCGCATCTTACAGATACAAAGTTGCTAACTGGGCATATCAAC 660
Db 601 GTCTGCTTAACCCCAATGAGCGCATCTTACAGATACAAAGTTGCTAACTGGGCATATCAAC 660
Oy 661 AGGTCCAAACAAATTAAGAAAGATGCTGATTTGAGCATGATGTTTGGAGATGGAATTT 720
Db 661 AGGTCCAAACAAATTAAGAAAGATGCTGATTTGAGCATGATGTTTGGAGATGGAATTT 720
Oy 721 ATGTGCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGATCAATCTATTC 780
Db 721 ATGTGCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGATCAATCTATTC 780
Oy 781 CATCTGTGAGTGACTCTTTGACATGAGAGAAATTTCTACTATATTCAGACAAAGCTAGAA 840
Db 781 CATCTGTGAGTGACTCTTTGACATGAGAGAAATTTCTACTATATTCAGACAAAGCTAGAA 840
Oy 841 TTGTTTCCCTTCTACTGGGCAATACACGCAATGATTTTGGCTGAAATTAAGTGAATAG 900
Db 841 TTGTTTCCCTTCTACTGGGCAATACACGCAATGATTTTGGCTGAAATTAAGTGAATAG 900
Oy 901 AATTAATAACAATTTGATATGATATACCTCCCACTTTTATGATGCTGTTTCCCTTCAA 960
Db 901 AATTAATAACAATTTGATATGATATACCTCCCACTTTTATGATGCTGTTTCCCTTCAA 960
Oy 961 TTGTTGCTGATATTTAATAAAGCATATCTATTCCTGCAATGTTGAGGAAGATATCTGA 1020
Db 961 TTGTTGCTGATATTTAATAAAGCATATCTATTCCTGCAATGTTGAGGAAGATATCTGA 1020
Oy 1021 AGATTAGACATGTTGGGAAGACGTACCAAAATTAACAAAATGAGATATGTTCCAGT 1080
Db 1021 AGATTAGACATGTTGGGAAGACGTACCAAAATTAACAAAATGAGATATGTTCCAGT 1080
Oy 1081 TGTAGAAATTAAGTGTACACATTTTGTGTAATTAATTAATTTTATTCACCAACATTT 1140
Db 1081 TGTAGAAATTAAGTGTACACATTTTGTGTAATTAATTAATTTTATTCACCAACATTT 1140
Oy 1141 TCAAGTTTGTATTTGTTAATAAATGATTATTCAGGAAAAAATTTTTTTT 1195
Db 1141 TCAAGTTTGTATTTGTTAATAAATGATTATTCAGGAAAAAATTTTTTTT 1195

RESULT 11
ADG26744 ID ADG26744 standard; cDNA; 1195 BP.
AC ADG26744;
XX
XX 26-FEB-2004 (first entry)
XX
```

DE Human prostate-specific cDNA #678.
 XX Human: prostate-specific polypeptide; gene; ss; prostate cancer;
 KM cytosolic.
 XX Homo sapiens.
 OS
 XX US2003157089-A1.
 PN
 XX 21-AUG-2003.
 PD
 PF 09-MAY-2002; 2002US-00144678.
 XX
 XX 25-FEB-1997; 97US-00806099.
 PR 01-AUG-1997; 97US-00904804.
 PR 09-FEB-1998; 98US-00020956.
 PR 25-FEB-1998; 98US-00030607.
 PR 14-JUL-1998; 98US-00115453.
 PR 23-SEP-1998; 98US-00159812.
 PR 15-JAN-1999; 99US-00232149.
 PR 09-APR-1999; 99US-00288946.
 PR 13-JUL-1999; 99US-00352616.
 PR 12-NOV-1999; 99US-00439313.
 PR 18-NOV-1999; 99US-00443686.
 PR 14-JAN-2000; 2000US-00483672.
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00568100.
 PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605783.
 PR 09-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 02-OCT-2000; 2000US-00679426.
 PR 10-OCT-2000; 2000US-00685168.
 PR 09-NOV-2000; 2000US-00709729.
 PR 12-JAN-2001; 2001US-00759143.
 PR 09-FEB-2001; 2001US-00780669.
 PR 09-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-00895814.
 PR 10-DEC-2001; 2001US-00012896.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
 PI Kales MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
 PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
 PI McNeill PD, Houghton RL, Vinals Y De Bassolis, Foy TM, Matanabe Y;
 PI Meagher MJ, Deng T;
 XX
 XX WPI: 2003-777973/73.
 DR P-PsDB; ADG26745.
 XX
 XX New polynucleotides encoding prostate specific polypeptides isolated from
 PT a human prostate tumor cDNA library are useful to diagnose and treat
 XX cancer particularly prostate cancer.
 XX
 PS Example 5; SEQ ID NO 878; 99pp; English.
 XX
 XX The invention relates to human prostate-specific polypeptides and the
 CC polynucleotides encoding them. The invention also relates to an isolated
 CC antibody or its antigen-binding fragment that specifically binds a
 CC polypeptide of the invention, a method of detecting cancer in a patient
 CC comprising contacting a biological sample of the patient with an agent
 CC that binds a prostate-specific polypeptide and comparing the amount of
 CC bound polypeptide compared to a predetermined cut-off value and a fusion
 CC protein comprising a prostate-specific polypeptide. The sequences of the
 CC invention are used to diagnose and treat cancer, particularly prostate
 CC cancer. This sequence represents cDNA encoding a human prostate-specific
 CC polypeptide of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format directly from USPTO at seqdata.uspto.gov/sequence.html.
 XX

50 Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other:

Query Match 100.0%; Score 1195; DB 10; Length 1195;
 Best Local Similarity 100.0%; Pred. No. 4,4e-276;
 Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CCGAGACTCAGCGTCAAGCTTAAGGCGAAGTGGGTGGCTGAAGCCATATCTTTTAG	60
DB	1	CCGAGACTCAGCGTCAAGCTTAAGGCGAAGTGGGTGGCTGAAGCCATATCTTTTAG	60
QY	61	AATTATGAAAGCAGAAAGACATCAAAACCAAGAAAGACTTTGGAAATGAAGCTTA	120
DB	61	AATTATGAAAGCAGAAAGACATCAAAACCAAGAAAGACTTTGGAAATGAAGCTTA	120
QY	121	GGAGAAATTTAGAAAGAGCATTTATTTGCTTAAGACAGGGGAGAACCGCATGCTTA	180
DB	121	GGAGAAATTTAGAAAGAGCATTTATTTGCTTAAGACAGGGGAGAACCGCATGCTTA	180
QY	181	AAAGACCTGTCTTTTGCAATTTGACCAACAGCCCATGCTGATGAATTTGACTGCCCTT	240
DB	181	AAAGACCTGTCTTTTGCAATTTGACCAACAGCCCATGCTGATGAATTTGACTGCCCTT	240
QY	241	CAGAACTTCAGACACACAGAACTCTTCCACAGTGGCACTTSCCAATTTAAATAGCTG	300
DB	241	CAGAACTTCAGACACACAGAACTCTTCCACAGTGGCACTTSCCAATTTAAATAGCTG	300
QY	301	CTATTATGACATCTCTGACCTTTCTTTTCACTCTTTGAGGAGATTAATACCTTTAG	360
DB	301	CTATTATGACATCTCTGACCTTTCTTTTCACTCTTTGAGGAGATTAATACCTTTAG	360
QY	361	CAACTCCCATCAACAAATTTTATTAATAATCCAACTGGTCAACAAGCTTTGC	420
DB	361	CAACTCCCATCAACAAATTTTATTAATAATCCAACTGGTCAACAAGCTTTGC	420
QY	421	CAATGTTTCCATCATCTCTGCGATTTGTTTACCTGCGAGTGTGATACAGCAATTG	480
DB	421	CAATGTTTCCATCATCTCTGCGATTTGTTTACCTGCGAGTGTGATACAGCAATTG	480
QY	481	TCCAACTTCATPATGAAGCAAGTATAGAAATTTCCACATTTGGTGAATAAGTGATG	540
DB	481	TCCAACTTCATPATGAAGCAAGTATAGAAATTTCCACATTTGGTGAATAAGTGATG	540
QY	541	TAAAGAAAGAGAGTTGGGGCTCTCAGTTCTTTTGTCTGTAATGCAATTTATA	600
DB	541	TAAAGAAAGAGAGTTGGGGCTCTCAGTTCTTTTGTCTGTAATGCAATTTATA	600
QY	601	GTCGTCTTACCCCAATGAGGCGATCTCAAGATACAGTGTCTTAACTGGGCAATTCAC	660
DB	601	GTCGTCTTACCCCAATGAGGCGATCTCTACAGATACAGTGTCTTAACTGGGCAATTCAC	660
QY	661	AGGTCCAAACAAATTAAGAAAGATGCTGTGATTTGACATGATCTTTGGAAATGAGATTT	720
DB	661	AGGTCCAAACAAATTAAGAAAGATGCTGTGATTTGACATGATCTTTGGAAATGAGATTT	720
QY	721	ATGTGCTCTGGGAATTTGGGATTTGGCAATCTGGCTGTGTTGGCTGTGACATCTATTC	780
DB	721	ATGTGCTCTGGGAATTTGGGATTTGGCAATCTGGCTGTGTTGGCTGTGACATCTATTC	780
QY	781	CATCTGTAGTACTCTTTGACATGAGAAATTTCACTATATTAAGACAACTTAGAA	840
DB	781	CATCTGTAGTACTCTTTGACATGAGAAATTTCACTATATTAAGACAACTTAGAA	840
QY	841	TTGTTTCCCTTTACTGGGCAATTAACAGCATTTTGGCTGGAATTAAGTGATG	900
DB	841	TTGTTTCCCTTTACTGGGCAATTAACAGCATTTTGGCTGGAATTAAGTGATG	900
QY	901	ATATTAACAAATTTGATGATGATACACCTCCCACTTTTATGATGCTTTCTTCCA	960
DB	901	ATATTAACAAATTTGATGATGATACACCTCCCACTTTTATGATGCTTTCTTCCA	960
QY	961	TTGTTTCCCTTTACTGGGCAATTAACAGCATTTTGGCTGGAATTAAGTGATG	1020
DB	961	TTGTTTCCCTTTACTGGGCAATTAACAGCATTTTGGCTGGAATTAAGTGATG	1020

QY 481 TCCAGCTTATATGGAACCAAGTATAGAAAGTTTCCAGATGGTTGATAGTGGATGT 540
 DB 481 TCCAGCTTATATGGAACCAAGTATAGAAAGTTTCCAGATGGTTGATAGTGGATGT 540
 QY 541 TAAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTGTCTGACTGATGCAATTATTA 600
 DB 541 TAAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTGTCTGACTGATGCAATTATTA 600
 QY 601 GTCTGCTTACCAATGAGGCGCATCTTACAGATACAAAGTTGCTAACTGGGCAATTAAC 660
 DB 601 GTCTGCTTACCAATGAGGCGCATCTTACAGATACAAAGTTGCTAACTGGGCAATTAAC 660
 QY 661 AGGTCCAAAGAAATAAGAGATGCTGAGATGATGATGATGATGATGATGATGATGATG 720
 DB 661 AGGTCCAAAGAAATAAGAGATGCTGAGATGATGATGATGATGATGATGATGATGATG 720
 QY 721 ATGTGCTCTGGGAATTTGGGATTTGGCAATATGAGCTGCTGTTGGCTGATCTATTC 780
 DB 721 ATGTGCTCTGGGAATTTGGGATTTGGCAATATGAGCTGCTGTTGGCTGATCTATTC 780
 QY 781 CATCTGTGAGTACTCTTTGACATGAGAAATTTTCACTATATTCAGAGCAAGCTAGAA 840
 DB 781 CATCTGTGAGTACTCTTTGACATGAGAAATTTTCACTATATTCAGAGCAAGCTAGAA 840
 QY 841 TTGTTTCCCTTCTACTGGGACAAATACAGCAATGATTTTGGCTGGAATTAAGTGAATG 900
 DB 841 TTGTTTCCCTTCTACTGGGACAAATACAGCAATGATTTTGGCTGGAATTAAGTGAATG 900
 QY 901 ATATTAACAATTTGTATGATATACACTTCACTTTTATGATAGCTGTTTCTTCCA 960
 DB 901 ATATTAACAATTTGTATGATATACACTTCACTTTTATGATAGCTGTTTCTTCCA 960
 QY 961 TTGTTTCTCTGATTTTAAAGATCTATCTCTGCAATGCTTGAAGAAAGATATCTGA 1020
 DB 961 TTGTTTCTCTGATTTTAAAGATCTATCTCTGCAATGCTTGAAGAAAGATATCTGA 1020
 QY 1021 AGATTAGACATGGTTGGGAAGAGCTGACCAAAATTAACAAACCTGAGATGTTCCAGT 1080
 DB 1021 AGATTAGACATGGTTGGGAAGAGCTGACCAAAATTAACAAACCTGAGATGTTCCAGT 1080
 QY 1081 TGTAGATTTACTGTTTACACACATTTTGTTCATATATGATATTTTATCACCAACAT 1140
 DB 1081 TGTAGATTTACTGTTTACACACATTTTGTTCATATATGATATTTTATCACCAACAT 1140
 QY 1141 TCAAGTTTGTATTTGTTAATTAATGATTTTCAAGGAAAAAATTTTAAAAA 1195
 DB 1141 TCAAGTTTGTATTTGTTAATTAATGATTTTCAAGGAAAAAATTTTAAAAA 1195
 RESULT 14
 ADP88258 standard; cDNA; 1195 BP.
 AC ADP88258;
 XX 12-AUG-2004 (first entry)
 DE Prostate cancer marker gene STEAP, SEQ ID NO:35.
 KW Diagnostic marker; portfolio; diagnostic parameter; gene expression;
 KW relative expression; heuristic rule; molecular diagnostic; diagnosis;
 KW prognosis; cancer; breast; prostate; ovarian; colorectal; lung;
 KW screening portfolio; human; STEAP; gene; ss.
 OS Homo sapiens.
 XX EP1349104-A2.
 PN 01-OCT-2003.
 PD 31-MAR-2003; 2003BP-00252027.
 PF
 XX

PR 29-MAR-2002; 2002US-0368790P.
 XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 XX
 XX Jackoe T;
 PI
 DR WPI; 2003-815043/77.
 XX
 PT Selecting a portfolio of markers useful in diagnostic applications
 PT comprises defining diagnostic parameters and establishing a relationship
 PT among the diagnostic parameters that identifies an optimized portfolio of
 PT markers.
 PS
 PS Example 2; SEQ ID NO 35; 154bp; English.
 XX
 CC The invention relates to a method of selecting a portfolio of markers
 CC (e.g., genes) for use in a diagnostic application. The method involves:
 CC (a) defining diagnostic parameters; (b) establishing a relationship among
 CC the diagnostic parameters so that they are optimized; and (c) selecting
 CC the optimal group of markers (the portfolio) for the diagnostic
 CC application. The diagnostic parameters can include a measure of the
 CC relative degree of expression of a gene, a measure of the variation in
 CC the measurement of the degree of gene expression, and the relationship
 CC between the diagnostic and discriminating parameters can be a mean
 CC variance relationship. The method further comprises the application of a
 CC heuristic rule. The invention also relates to a general-purpose computer
 CC programmed to identify a portfolio of markers, instructions for
 CC performing the method of the invention, and a diagnostic portfolio
 CC comprising genes selected according to the method. The method of the
 CC invention can be used in conjunction with any method for determining the
 CC gene expression of relevant cells as well as protein-based methods of
 CC determining gene expression. The method of the invention can be used in
 CC screening, diagnosing and prognosing diseases associated with changes in
 CC the expression of multiple genes (e.g., breast, prostate, ovarian,
 CC colorectal or lung cancer). By grouping these markers into portfolios,
 CC the most reliable results can be obtained with the smallest number of
 CC markers necessary to obtain such a result, which is particularly
 CC important in multiple-step assays such as nucleic acid amplification methods.
 CC The present sequence represents a human diagnostic marker gene that is a
 CC member of an optimized portfolio of 31 genes for screening for prostate,
 CC breast, colon, ovarian and lung cancer.
 CC
 XX
 SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1195; DB 11; Length 1195;
 Best Local Similarity 100.0%; Pred. No. 4.4e-276;
 Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGAGACTCACCGTCAAGCTAAGGCGAAGTGGTGGCTGAAGCCATATTTATATG 60
 DB 1 CCGAGACTCACCGTCAAGCTAAGGCGAAGTGGTGGCTGAAGCCATATTTATATG 60
 QY 61 AATTAAATGGAAGCAGAAAAAGACATCAAAACCAAGAAACCTTTGGAAAAATGAAGCTTA 120
 DB 61 AATTAAATGGAAGCAGAAAAAGACATCAAAACCAAGAAACCTTTGGAAAAATGAAGCTTA 120
 QY 121 GGAGAAATTTAAGAGAGAGCATTTTTCATTAAGGACAGGAGAGACAGCATGCTTA 180
 DB 121 GGAGAAATTTAAGAGAGAGCATTTTTCATTAAGGACAGGAGAGACAGCATGCTTA 180
 QY 181 AAAGACTGTGCTTTTGGCATTTTGCACAAAGCCCATGCTGATGATTTGAATGAGCTT 240
 DB 181 AAAGACTGTGCTTTTGGCATTTTGCACAAAGCCCATGCTGATGATTTGAATGAGCTT 240
 QY 241 CAGAACTTACAGACACACAGAACTTTTCCACAGTGGCATTTGCCAATTAATATGCTG 300
 DB 241 CAGAACTTACAGACACACAGAACTTTTCCACAGTGGCATTTGCCAATTAATATGCTG 300
 QY 301 CTATTATAGCATCTGCACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCTTTAG 360
 DB 301 CTATTATAGCATCTGCACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCTTTAG 360
 QY 361 CAATTCCTCATCAACATATTTTATTAATTCATCTGCTGATCAACAAAGTCTTGC 420

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Db ||||| 361 CAACCTCCCATCAACAATATTTTATMAAATCCAACTCGTCAATCAACAAAGCTTGC 420
Qy ||||| 421 CAATGTTTCACTGCTCTTGSCATGTTTACTGCGAGTGTGATAGCAATTTG 480
Db ||||| 421 CAATGTTTCACTGCTCTTGSCATGTTTACTGCGAGTGTGATAGCAATTTG 480
Qy ||||| 481 TCCAACTTCATTAATGGAACCAAGTATAGAAATTTCCAACTGTTGATAGTGAATGT 540
Db ||||| 481 TCCAACTTCATTAATGGAACCAAGTATAGAAATTTCCAACTGTTGATAGTGAATGT 540
Qy ||||| 541 TTAACAAGAAAGCAATTTGGGCTTCTCACTTTCTTTTCTGCTACTGCAATTTATTA 600
Db ||||| 541 TTAACAAGAAAGCAATTTGGGCTTCTCACTTTCTTTTCTGCTACTGCAATTTATTA 600
Qy ||||| 601 GTCTGCTTACCCAAATGAGGCAATCTTAAGATACAAAGTTGCTAACTGGGCAATCAAC 660
Db ||||| 601 GTCTGCTTACCCAAATGAGGCAATCTTAAGATACAAAGTTGCTAACTGGGCAATCAAC 660
Qy ||||| 661 AGGTCCAAACAAATTAAGAAAGATGCTGATGAGCATGATGTTTGAGAAATGAGATTT 720
Db ||||| 661 AGGTCCAAACAAATTAAGAAAGATGCTGATGAGCATGATGTTTGAGAAATGAGATTT 720
Qy ||||| 721 ATGTGCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGTGACATCTATTC 780
Db ||||| 721 ATGTGCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGTGACATCTATTC 780
Qy ||||| 781 CATCTGTAGTACTCTTTGACATGAGAAATTTTACTATTAATGAGCAAGTATGGA 840
Db ||||| 781 CATCTGTAGTACTCTTTGACATGAGAAATTTTACTATTAATGAGCAAGTATGGA 840
Qy ||||| 841 TTGTTTCCCTTCTACTGCGCACATPACAGCATTTGTTTCTGCTGAAATTAAGTGAATG 900
Db ||||| 841 TTGTTTCCCTTCTACTGCGCACATPACAGCATTTGTTTCTGCTGAAATTAAGTGAATG 900
Qy ||||| 901 ATATTAACAAATTTGATGATGATACACCTCCAACTTTATGATGATGTTTCTTCCAA 960
Db ||||| 901 ATATTAACAAATTTGATGATGATACACCTCCAACTTTATGATGATGTTTCTTCCAA 960
Qy ||||| 961 TTGTTGCTCTGATATTTAAAGCACTATTCCTGCGCATGTTGAGAAAGATATCTGA 1020
Db ||||| 961 TTGTTGCTCTGATATTTAAAGCACTATTCCTGCGCATGTTGAGAAAGATATCTGA 1020
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Db ||||| 1021 AGATTAGACATGTTGGGAAGAGCTGACCAAAATTAACAAAATGAGATATGTTCCAGT 1080
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XX
XX ADL06462;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human tumour-associated antigenic target (TAT) cDNA sequence #42.
XX
XX Human; tumour-associated antigenic target; TAT; cell death; tumour;
XX
XX cancer; cytosolic; gene; ss.
XX
XX Homo sapiens.
XX
XX WO2004016225-A2.
XX
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PD 26-FEB-2004.
XX
XX 19-AUG-2003; 2003WO-US025892.
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XX 19-AUG-2002; 2002US-0404809P.
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XX 02-JUL-2003; 2003US-0484959P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;
XX
XX Spencer SD, Wu TD, Zhang Z;
XX
XX WPI; 2004-257144/24.
XX
XX P-PSDB; ADL06542.
XX
XX New antibody that binds to a tumor-associated antigenic target (TAT)
XX
XX polypeptide, useful for preparing a composition for diagnosing or
XX
XX treating cancer.
XX
XX Claim 1; SEQ ID NO 42; 319pp; English.
XX
XX The present invention relates to the isolation of human tumour-associated
XX
XX antigenic target (TAT) polynucleotide and polypeptide sequences. Also
XX
XX disclosed is an antibody that binds to a TAT polypeptide. The antibody is
XX
XX a monoclonal antibody, an antibody fragment, a chimeric antibody or a
XX
XX humanized antibody. It is conjugated to a growth inhibitory agent. It is
XX
XX produced in bacteria or in CHO cells and induces death of a cell to which
XX
XX it binds. The antibody is useful for preparing a composition for
XX
XX diagnosing or treating tumours and cancer. The present sequence
XX
XX represents a human TAT cDNA sequence of the invention.
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XX Best Local Similarity 100.0%; Pred. No. 4,4e-276; Indels 0; Gaps 0;
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Search completed: December 4, 2005, 21:08:41
Job time : 807.249 secs

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LOCUS AR366780 Sequence 1 from patent US 6329503.

ACCESSION AR366780
VERSION AR366780.1 GI:3459746
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1195)
AUTHORS Afar,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and Mitchell,S.C.
TITLE Serpentine transmembrane antigens expressed in human cancers and uses thereof
JOURNAL Patent: US 6329503-A 1 11-DEC-2001;
Agensys, Inc.; Santa Monica, Ca;
WOX;
FEATURES
source Location/Qualifiers
1..1195
/organism="unknown"
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Query Match 100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 5-5e-238;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
AR405830 1195 bp DNA linear PAT 18-DEC-2003

LOCUS AR405830
DEFINITION Sequence 878 from patent US 6630305.
ACCESSION AR405830
VERSION AR405830.1 GI:40154667

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1195)

AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kaijoh, M.D., Ranger, G.R., Retzer, M.W., Skolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,
Hepler, W.T. and Henderson, R.A.

TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer

JOURNAL Patent: US 6630305-A 878 07-OCT-2003;
Corixa Corporation, Seattle, WA;
WOX;

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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.5e-238;
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RESULT 4
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LOCUS AR564210

DEFINITION Sequence 878 from patent US 6759515.
ACCESSION AR564210
VERSION AR564210.1 GI:53979261
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1195)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6759515-A 878 06-JUL-2004;
Corixa Corporation; Seattle, WA
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Best Local Similarity 100.0%; Pred. No.5.5e-238;
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LOCUS AR589196
DEFINITION Sequence 878 from patent US 6800746.
ACCESSION AR589196
VERSION AR589196.1 GI:56636093
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1195)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6800746-A 878 05-OCT-2004;
Corixa Corporation; Seattle, WA
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/organism="unknown"
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Query Match 100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No.5.5e-238;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DEFINITION Sequence 1 from patent US 6887975.
 ACCESSION AR654075
 VERSION AR654075.1 GI:67584962
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1195)
 AUTHORS Afari, D.E., Hubert, R.S., Leong, K., Raitano, A.B., Saffran, D.C. and Mitchell, S.C.
 TITLE Peptides derived from STEAP1
 JOURNAL Patent: US 6887975-A 1 03-MAY-2005;
 Agencies, Inc.; Santa Monica, CA
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Query Match 100.0%; Score 1195; DB 6; Length 1195;
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RESULT 7
AX201105 1195 bp DNA linear PAT 29-AUG-2001
LOCUS Sequence 735 from Patent WO0151633.
DEFINITION AX201105
ACCESSION AX201105
VERSION AX201105.1 GI:15390890
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 735 19-JUL-2001;
CORIXA CORPORATION (US)
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Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX267904 1195 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 878 from Patent WO0173032.
ACCESSION AX267904
VERSION AX267904.1 GI:16516522
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homnidae; Homo.
REFERENCE
1 Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y.,
Kelso, M. D., Fanger, G. R., Rether, M. W., Stolk, J. A., Day, C. H.,
Vedvick, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A., Hepfler, W. T.,
and Henderson, R. A.
Compositions and methods for the therapy and diagnosis of prostate
cancer.
Patent: WO 0173032-A 878 04-OCT-2001;
JOURNAL CORIXA CORPORATION (US)
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Query Match 100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 5.5e-238; Mismatches 0; Indels 0; Gaps 0;
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ACCESSION AX926483
VERSION AX926483.1 GI:40246089
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Wang, Y.
Panel of nucleic acid sequences for cancer diagnosis
Patent: EP 1351510-A 35 22-OCT-2003;
JOURNAL Ortho-Clinical Diagnostics, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 5.5e-238; Mismatches 0; Indels 0; Gaps 0;
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OY	361	CAACTTCCCATCAACAATATTTTATATAAATTCCAATCTCGTCAATCAACAAAGTCTTGC	420
Db	361	CAACTTCCCATCAACAATATTTTATATAAATTCCAATCTCGTCAATCAACAAAGTCTTGC	420
OY	421	CAATGGTTTCATCACTCTCTGGCAATGCTTACCTGCGAGGTGATPAGCAGCAATTG	480
Db	421	CAATGGTTTCATCACTCTCTGGCAATGCTTACCTGCGAGGTGATPAGCAGCAATTG	480
OY	481	TCCAACTTCATATATGGAACCAAGTATPAGAAGTTTCCACATTGGTTGATPAAGTGATGT	540
Db	481	TCCAACTTCATATATGGAACCAAGTATPAGAAGTTTCCACATTGGTTGATPAAGTGATGT	540
OY	541	TAAACAAGAAAGCAATTTGGGCTTTCACAGTTCTTTTTCCTGTAACGTGCATATTA	600
Db	541	TAAACAAGAAAGCAATTTGGGCTTTCACAGTTCTTTTTCCTGTAACGTGCATATTA	600
OY	601	GTCCTCTCTTAACTCCCAATGAGGCGATCCTACAGATACAAAGTGGCTAAACCTGGCATATCAAC	660
Db	601	GTCCTCTCTTAACTCCCAATGAGGCGATCCTACAGATACAAAGTGGCTAAACCTGGCATATCAAC	660
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Db	661	AGGTCCAAACAAATTAAGAAGATGCTCTGATTTGAGCATGATGTTTGGAGATGGAGATTT	720
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Db	901	ATATATAAACAAATTTGATGATGTATACACCTTCAACTTTTATGATAGCTGTTTTCTTCCA	960
OY	961	TTGTTGTCTGATATTTAAAGACATCTATTTCTGCGCATGCTTGAGAGAGAAATACTGA	1020
Db	961	TTGTTGTCTGATATTTAAAGACATCTATTTCTGCGCATGCTTGAGAGAGAAATACTGA	1020
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Db	1021	AATTTAGACATGTTGGGAAGACGTACCAAAATTAACAAACTGAGATPAGTGTCCAGT	1080
OY	1081	TGTAGAAATTAAGTTTACACATTTTGTGTAATATGATATATTTTATACCAACATTT	1140
Db	1081	TGTAGAAATTAAGTTTACACATTTTGTGTAATATGATATATTTTATACCAACATTT	1140
OY	1141	TCAAAGTTTGTATTTGTTAATAAATGATATTTCAAAGAAAAAATTTTTTTTTTTTTTTT	1195
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LOCUS	AX951736	1195 bp	DNA	linear	PAT 08-JAN-2004
DEFINITION	Sequence 35 from Patent EP1367138.				
ACCESSION	AX951736				
VERSION	AX951736.1	GI:40782084			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Wang, Y.				
JOURNAL	Markers for breast cancer prognosis				
FEATURES	Patent: EP 1367138-A 35 03-DEC-2003; Ortho Clinical Diagnostics Inc. (US)				
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QY	61	AATTATGGAAGAGCAAAAGACATCACAAACCAAGAACTTTGGAAATGAAAGCTTA	120		
DB	61	AATTATGGAAGAGCAAAAGACATCACAAACCAAGAACTTTGGAAATGAAAGCTTA	120		
QY	121	GGAGAAATTTGAAGAAGACATATTATTTGCATTAAGGACAGCGGAGAGACAGCATGTCTAA	180		
DB	121	GGAGAAATTTGAAGAAGACATATTATTTGCATTAAGGACAGCGGAGAGACAGCATGTCTAA	180		
QY	181	AAAGACCTGTGCTTTTGGCATTTGACCAAAAGAGCCATGCTGATGAATTTGACTGCCCTT	240		
DB	181	AAAGACCTGTGCTTTTGGCATTTGACCAAAAGAGCCATGCTGATGAATTTGACTGCCCTT	240		
QY	241	CAGAACTTCAGACACACAGAAACCTTTTCCAGAGTGGCACTTGCATTTAAATATAGCTG	300		
DB	241	CAGAACTTCAGACACACAGAAACCTTTTCCAGAGTGGCACTTGCATTTAAATATAGCTG	300		
QY	301	CTATTATGACACTCTGTGACTTTTCTTCACTCTTCTGAGGAAATTCACCCCTTAG	360		
DB	301	CTATTATGACACTCTGTGACTTTTCTTCACTCTTCTGAGGAAATTCACCCCTTAG	360		
QY	361	CAACTTCCATCAACAATATTTTATTAATTCATCTGTGATCAACAAAGTCTTGC	420		
DB	361	CAACTTCCATCAACAATATTTTATTAATTCATCTGTGATCAACAAAGTCTTGC	420		
QY	421	CAATGTTTCCATCACTCTCTTGGATTTGATTACCTGACAGTGTGATAGCAGCAATTG	480		
DB	421	CAATGTTTCCATCACTCTCTTGGATTTGATTACCTGACAGTGTGATAGCAGCAATTG	480		
QY	481	TCCAATTCATTAATGGAACCAAGTATTAAGAGTTTCCATTTGTTGATTAAGTGAATGT	540		
DB	481	TCCAATTCATTAATGGAACCAAGTATTAAGAGTTTCCATTTGTTGATTAAGTGAATGT	540		
QY	541	TAAACAAGAAAGAGTTTGGGCTTCTCAAGTTCTTTTGGTCTGACTGATGCAATTTATA	600		
DB	541	TAAACAAGAAAGAGTTTGGGCTTCTCAAGTTCTTTTGGTCTGACTGATGCAATTTATA	600		
QY	601	GTCTGTCTTAACCAATGAGGAGCATCTCAGATACAAAGTTGCTTAACTGGGACATATCAAC	660		
DB	601	GTCTGTCTTAACCAATGAGGAGCATCTCAGATACAAAGTTGCTTAACTGGGACATATCAAC	660		

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RESULT 11

AX960014 1195 bp DNA linear PAT 14-JAN-2004

LOCUS AX960014
DEFINITION Sequence 35 from Patent EP1349104.
ACCESSION AX960014
VERSION AX960014.1 GI:40880240
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1
AUTHORS Jatkoe, T.
TITLE Method of selecting a portfolio of markers for use in a diagnostic
JOURNAL application
Patent: EP 1349104-A 35 01-OCT-2003;
FEATURES Ortho-Clinical Diagnostics, Inc. (US)
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ORIGIN

Query Match 100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 5.5e-238;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CCGAGACTCAGCTCAAGCTTAAGCGAAGAGTGGTGGCTGAAGCCATATCTATTTATAG 60
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DEFINITION   (STEAP1) mRNA, complete cds.
ACCESSION    AF186249
KEYWORDS     AF186249.1 GI:6572947
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE    1 (bases 1 to 1195)
AUTHORS      Hubert,R.S., Vivanco,I., Chen,E., Rastegar,S., Leong,K.,
              Mitchell,S.C., Madraswala,R., Zhou,Y., Kuo,D., Raitano,A.B.,
              Jakobovits,A., Saffran,D.C. and Afari,D.E.
              STEAP: a prostate-specific cell-surface antigen highly expressed in
              human prostate tumors
              Proc. Natl. Acad. Sci. U.S.A. 96 (25), 14523-14528 (1999)
JOURNAL      PubMed
PUBMED       10588738
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AUTHORS      Hubert,R.S., Vivanco,I., Chen,E., Rastegar,S., Leong,K.,
              Mitchell,S.C., Madraswala,R., Zhou,Y., Kuo,D., Raitano,A.B.,
              Jakobovits,A., Saffran,D.C. and Afari,D.E.H.
              Direct Submission
              Submitted (14-SEP-1999) UroGeneys Inc., 1701 Colorado Ave., Santa
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Query Match      100.0%; Score 1195; DB 8; Length 1195;
Best Local Similarity 100.0%; Pred. No. 5,5e-238;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS        CO981397
DEFINITION   Sequence 252 from Patent Epi498424.
ACCESSION    CO981397
VERSION      CO981397.1 GI:58190687
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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
1
AUTHORS Rosenthal, A., Hermann, K., Heiden, E., Pilarek, C., Bruemendorf, T.,
Straub, B., Roepcke, S., Mennerich, D., Kimmern, H. and Li, X.
TITLE Human nucleic acid sequences from lung tumours
JOURNAL Patent: EP 1498424-A 252 19-JAN-2005;
Hinzmann, Bernd (DE); Hermann, Klaus (DE); Heiden, Esméralda (DE);
Rosenthal, Andre (DE)
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Best Local Similarity 100.0%; Pred. No. 5.4e-238; Mismatches 0; Gaps 0;
Matches 1195; Conservative 0; Indels 0; Gaps 0;

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1216 TGTAGAAATTAAGTGTGTTTACACATTTTGTCAATATTGATATTTTATCACCAATTT 1275
1141 TCAAGTTTGTATTTGTTTATATAAATGATTTTCAAGAGAAAAAATTTTAAAAA 1195
1276 TCAAGTTTGTATTTGTTTATATAAATGATTTTCAAGAGAAAAAATTTTAAAAA 1330

RESULT 14
CS031875 1330 bp DNA linear PAT 10-MAR-2005
LOCUS CS031875
DEFINITION Sequence 1381 from Patent WO2005016962.
ACCESSION CS031875
VERSION CS031875.1 GI:60731699
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
1
AUTHORS Abbas, A., Clark, H., Ouyang, W., Williams, M. P., Wood, W. I. and Wu, T. D.
TITLE Compositions and methods for the treatment of immune related diseases
JOURNAL Patent: WO 2005016962-A 1381 24-FEB-2005;
Genentech, Inc. (US)
FEATURES
source 1..1330
location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 1195; DB 6; Length 1330;
Best Local Similarity 100.0%; Pred. No. 5.4e-238; Mismatches 0; Gaps 0;
Matches 1195; Conservative 0; Indels 0; Gaps 0;

1 CCGAGACTCAGCGTCAAGCTAAGCGGAAGTGGGCTGAGCCATCTATTATTATAG 60
136 CCGAGACTCAGCGTCAAGCTAAGCGGAAGTGGGCTGAGCCATCTATTATTATAG 195
61 AATTAATGAAAGAGAGAAAGACATCAAAACCAAGAAACCTTTGAAAAATGAACTTA 120
196 AATTAATGAAAGAGAGAAAGACATCAAAACCAAGAAACCTTTGAAAAATGAACTTA 255
121 GGAGAAATTTAGAGAGAGAGATTTTGTGCTAAGAGAGAGAGAGAGAGAGAGAGAGAG 180
256 GGAGAAATTTAGAGAGAGAGATTTTGTGCTAAGAGAGAGAGAGAGAGAGAGAGAGAG 315

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 03:12:22 ; Search time 376.544 Seconds
(without alignments)
987.668 Million cell updates/sec

Title: US-10-750-262-1

Perfect score: 1195

Sequence: 1 ccgagactccagtcgaact.....ggaaaaaaaaaaaaaa 1195

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3289935 seqs, 155610033 residues

Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_NA_New:*
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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	3.3	1687	6	US-10-750-185-59979
2	39.2	3.3	1779	6	US-10-750-185-25365
3	39	3.3	2464	6	US-10-750-185-59315
4	38.6	3.2	2133	6	US-10-750-185-26044
5	38.6	3.2	319608	7	US-11-145-703-1
6	37.6	3.1	1301	6	US-10-750-185-36894
7	37.4	3.1	1443	6	US-10-750-185-57750
8	37	3.1	1495	6	US-10-750-185-52077
9	37	3.1	1798	6	US-10-750-185-51935
10	36.8	3.1	1835	6	US-10-750-185-46765
11	36.8	3.1	2081	6	US-10-750-185-51383
12	36.6	3.1	1620	6	US-10-750-185-52737
13	36.4	3.0	2948	7	US-11-099-691-32
14	36.2	3.0	1577	6	US-10-750-185-45671
15	36.2	3.0	1978	6	US-10-750-185-42808
16	36.2	3.0	2120	6	US-10-689-742-163
17	36.2	3.0	2787	6	US-10-750-185-25062
18	36.2	3.0	3334	6	US-10-821-234-152
19	36	3.0	872	6	US-10-750-185-49060
20	36	3.0	2126	6	US-10-909-125-809
21	35.8	3.0	1458	6	US-10-821-234-142
22	35.8	3.0	2509	6	US-10-750-185-27479
23	35.6	3.0	1751	6	US-10-750-185-35358

24	35.4	3.0	1646	6	US-10-750-185-41075	Sequence 41075, A
25	35.2	2.9	894	6	US-10-689-742-5	Sequence 5, Appl1
26	35.2	2.9	925	6	US-10-750-185-46490	Sequence 46490, A
27	35.2	2.9	1076	6	US-10-750-185-44612	Sequence 44612, A
28	35.2	2.9	1328	6	US-10-750-185-42494	Sequence 42494, A
29	35.2	2.9	1694	6	US-10-689-742-49	Sequence 49, Appl1
30	35	2.9	399	7	US-11-108-172-547	Sequence 517, App
31	35	2.9	1034	6	US-10-750-185-61634	Sequence 61634, A
32	35	2.9	2508	6	US-10-750-185-40261	Sequence 40261, A
33	34.8	2.9	1673	6	US-10-750-185-51951	Sequence 51951, A
34	34.6	2.9	1021	6	US-10-750-185-30460	Sequence 30460, A
35	34.6	2.9	1407	6	US-10-632-150-5	Sequence 5, Appl1
36	34.6	2.9	1407	7	US-11-073-457-5	Sequence 5, Appl1
37	34.6	2.9	1417	6	US-10-750-185-52014	Sequence 52014, A
38	34.4	2.9	2580	6	US-10-750-185-57482	Sequence 57482, A
39	34.4	2.9	149419	7	US-11-112-908-47	Sequence 49, Appl1
40	34.4	2.9	16611	7	US-11-112-908-50	Sequence 47, Appl1
41	34.4	2.9	170189	7	US-11-112-908-50	Sequence 50, Appl1
42	34.2	2.9	1012	6	US-10-750-185-54610	Sequence 54610, A
43	34.2	2.9	1974	6	US-10-750-185-63164	Sequence 63164, A
44	34.2	2.9	2906	6	US-10-131-826A-367	Sequence 367, App
45	34.2	2.9	3069	6	US-10-750-185-40313	Sequence 40313, A

ALIGNMENTS

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RESULT 1
US-10-750-185-59979/c
; Sequence 59979, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 59979
; LENGTH: 1687
; TYPE: DNA
; ORGANISM: Bovine 1986680802008
US-10-750-185-59979

Query Match
Best Local Similarity 55.9%; Pred. No. 1.3;
Matches 76; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1060 AAACGTGAGATGTCCTCCCACTTGTAGATTAAGTCTTACACACATTTTGTCAATTTG 1119
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QY 1120 ATATATTTTTCACCAACATTTCAAGTTTGTATTTTAAATGAATATTTCAAGAA 1179
Db 447 TTTCATCTTTTGCACATTTGTTTATTTGTTGTTTGTATTTAATTTAATTCGAAGAGA 388
QY 1180 AAAAAAAAAAAAAA 1195
Db 387 AGGAAAGAGAAAGAA 372

RESULT 2
US-10-750-185-25365
; Sequence 25365, Application US/10750185
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* PUBLICAT ION NO. US20050260603A1
 * GENERAL INFORMATION:
 * APPLICANT: MMI GENOMICS, INC.
 * APPLICANT: DENISE, Sue K.
 * APPLICANT: KERR, Richard
 * APPLICANT: ROSENFIELD, David
 * APPLICANT: HOLM, Tom
 * APPLICANT: BATES, Stephen
 * APPLICANT: FANTIN, Dennis
 * TITLE OF INVENTION: COMPOSITIONS FOR INFE
 * FILE REFERENCE: MM1100-2
 * CURRENT APPLICATION NUMBER: US/10/750,185
 * CURRENT FILING DATE: 2003-12-31
 * PRIOR APPLICATION NUMBER: US 60/437,482
 * PRIOR FILING DATE: 2002-12-31
 * NUMBER OF SEQ ID NOS: 64922
 * SOFTWARE: Patent version 3.1
 * SEQ ID NO 25365
 * LENGTH: 1779
 * TYPE: DNA
 * ORGANISM: Bovine 19866880604913
 * US-10-750-185-25365

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Qy	829	GCAAGCTAGGAATTTGTTCCCTTCTACTGGGACATATACGCATTTGATTTTGGCCGGA	888
Db	825	AAAGACATGACACTTACTCTTTTGGCTGGGAAATAGATTAATGATTTGTCTTTGT	884
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RESULT 3
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Sequence 39315, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OR INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 39315
LENGTH: 2464
TYPE: DNA
ORGANISM: Bovine
US-10-750-185-39315 19866881564211

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b	1748	AGAGAAAAGGGAAATTCGACATATTAATTAATCCATTCGTCAGTATATCTGCAGCTCAAT	1689	

QY	959	AATGTGTCCTGAAATTTTAAAGCAATATTCCTCCATGCTTGAGGAAGAATCT	1018
Db	1688	AACGCAAGCATGAATTTTGTCTCTCTCTGTCCTTTATATAGTTAAGGAACAAGA	1629
QY	1019	GAAGATTAGACATGTTGGGAAAGCAGCAACCAAAATTTAACAAACGTGAGATFATGCCA	1078
Db	1628	CAAGATGTTAAACCTGGGTAAAGAAATCATTTAAABAAAAACAACACATGTTTTCCTT	1565
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Db	1568	CTATTACAGTT	1558

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RESULT 4
US-10-750-185-26044
Sequence 26044, Application US/10750185
Publication NO. US2005026063A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26044
LENGTH: 2133
TYPE: DNA
ORGANISM: Bovine
US-10-750-185-26044 19866880786954

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Qy	975	TTTAAAGCATACTATTCCTGCGATCGTTAGAGAGAATAGTAAAGATTAGACATGCT	1034		
Db	822	TGACATATATTAATAATTTTCTTAACAATACAGAAATGTATATATATGAAAGTTCCCATCAT	881		
Qy	1035	TGGGAAGACGCTCACCAAAATTTAACAAAACCTGACATATGTTCCCACTGTGTAGAAATTACTGT	1094		
Db	882	ATTAACATATATCCAGAAATGTATATTAACAAAGAAATTTCCATATATTCAGAAATTAACGTG	941		
Qy	1095	TTACACACATTTTGTTCATATATGTGATATATTTTATCACCACAACTTTCAGATTGTGATTT	1154		
Db	942	TTCTTAAAAATTTGGTTTATATTTTTCATTTTTCATGTGATATTTTAAACATATAAATAT	1001		
Qy	1155	GTTAATTTAAATGA	1167		
Db	1002	GTAATTACTTTGA	1014		

RESULT 5
US-11-145-703-1/c
Sequence 1, Application US/114570303
Publication No. US2005026067A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya

```

APPLICANT: Bouguetieret, Lydie
APPLICANT: Bihain, Bernard
APPLICANT: Essioux, Laurent
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKS
FILE REFERENCE: 53.US16.DIV
CURRENT APPLICATION NUMBER: US/11/145,703
CURRENT FILING DATE: 2000-03-30
PRIORITY APPLICATION NUMBER: US/10/147,603
PRIORITY FILING DATE: 2000-03-30
PRIORITY APPLICATION NUMBER: 09/539,333
PRIORITY FILING DATE: 2000-03-30
PRIORITY APPLICATION NUMBER: US 60/126,903
PRIORITY FILING DATE: 1999-03-30
PRIORITY APPLICATION NUMBER: US 60/131,971
PRIORITY FILING DATE: 1999-04-30
PRIORITY APPLICATION NUMBER: US 60/132,065
PRIORITY FILING DATE: 1999-04-30
PRIORITY APPLICATION NUMBER: US 60/143,928
PRIORITY FILING DATE: 1999-07-14
PRIORITY APPLICATION NUMBER: US 60/145,915
PRIORITY FILING DATE: 1999-07-27
PRIORITY APPLICATION NUMBER: US 60/146,453
PRIORITY FILING DATE: 1999-07-29
PRIORITY APPLICATION NUMBER: US 60/146,452
PRIORITY FILING DATE: 1999-07-29
PRIORITY APPLICATION NUMBER: US 60/162,288
PRIORITY FILING DATE: 1999-10-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 234
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 319608
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc.feature
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FEATURE:
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LOCATION: 1108..1289
OTHER INFORMATION: exon A g35018 gene
FEATURE:
NAME/KEY: exon
LOCATION: 14877..14920
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LOCATION:	237406..237428
OTHER INFORMATION:	exon Nbis complement g34872 gene

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/ LOCATION: 240528..240617
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/ OTHER INFORMATION: exon M52 complement g34872 gene
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/ LOCATION: 240528..240824
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/ FEATURE:
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/ OTHER INFORMATION: exon M692 complement g34872 gene
/ FEATURE:
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/ LOCATION: 240528..241685
/ OTHER INFORMATION: exon M1 complement g34872 gene
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 240800..240993
/ OTHER INFORMATION: exon M51 complement g34872 gene
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 241686..243685
/ OTHER INFORMATION: 5'regulatory region g34872 gene
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 290652..292652
/ OTHER INFORMATION: 3'regulatory region g34665 gene
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Query Match 3.2%; Score 38.6; DB 7; Length 319608;

Best Local Similarity 48.1%; Pred. No. 25;

Matches 139; Conservative 0; Mismatches 149; Indels 1; Gaps 1;

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QY 905 AAAACAATTGGTATGATACACCTCCAACTTTTATCATAGCTGTTTCTTCCATTTGT 964
DB 13082 AAACCAACTGTTAAGTTTCTTTCACTGAGTTATGTGTCTTTTAAATCACATTGG 13023
QY 965 TGTCCTGATATTTAAAGCATCTATCTCCGTCATGCTTGAGGAAGAATAGTCAAGAT 1024
DB 13022 TGGAAATATGATGATATATACATATCATATATATATATATATATATATATAT 12963
QY 1025 TAGACATGTTGGAGACGTCACCAAAATTAACMAAAGTGAATATGTTCCAGTTGTA 1084
DB 12962 AAATTAATATATATATATATATATATATATATATATATATATATATATATAT 12903
QY 1085 GAATTAAGTTTACACACATTTTGTCAATATGATATATTTATATACCAACATTTCAA 1144
DB 12902 TATATATATATATATATATATATATATATATATATATATATATATATATAT 12844
QY 1145 GTTGTATTTGTTAATATATATATATATATATATATATATATATATATATATAT 1193
DB 12843 TTATATATATATATATATATATATATATATATATATATATATATATATAT 12795
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RESULT 6

US-10-750-185-36894/c

; Sequence 36894, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2

; CURRENT APPLICATION NUMBER: US/10/750,185

; PRIOR FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 36894

; LENGTH: 1301

; TYPE: DNA

; ORGANISM: Bovine

US-10-750-185-36894

19866881016886

Query Match 3.1%; Score 37.6; DB 6; Length 1301;

Best Local Similarity 61.0%; Pred. No. 4.6;

Matches 61; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

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DB 851 TGCAGACATTTAATCTCCAAAATGTGTTGTGTTAATTCCTCCAGATTGTTCT 792
QY 1156 TTTAATAATGATTATTCAGAAAAAATTTTATTTTATTTTATTTTATTTTATTT 1195
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RESULT 7

US-10-750-185-57750

; Sequence 57750, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2

; CURRENT APPLICATION NUMBER: US/10/750,185

; PRIOR FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 57750

; LENGTH: 1443

; TYPE: DNA

; ORGANISM: Bovine

US-10-750-185-57750

19866881229395

Query Match 3.1%; Score 37.4; DB 6; Length 1443;

Best Local Similarity 48.4%; Pred. No. 5.3;

Matches 104; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

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Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

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Db 1042 ATATATATATATTAATTATATTACTAAATAAAATGAGTACATAAAGAAAAAGTAAA 1098

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US-10-750-185-42808/c
Sequence 43908 Ann

Sequence 42808, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:

; GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.

APPLICANT: DENISE, Sue K.

APPLICANT: KERR, Richard
APPLICANT: ROSENER, David

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, LOU
APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: COMPOS

FILE REFERENCE: MM1100-2

! CURRENT APPLICATION NUMBER: US/10/750,185
! CURRENT FILING DATE: 2003.12.31

; CURRENT FILING DATE: 200
 ; PRIOR APPLICATION NUMBER:

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

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; SOFTWARE: PatentIn version 3.1
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; NUMBER OF DEG AD NOS: 87222
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SEQ ID NO 42808

LENGTH: 1978

TYPE: DNA

ORGANISM: BOV
; 10-750-195-438

US-10-750-185-42

Query Match

Query maccn	3.08%	30
Best Local Similarity	62.28%	Pr

Matches 74; Conservative 0;

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Db 1509 CAATAGGGA TTTCAATTC TTAAGAGTCTTATTTTGC CAGAACCAAAAAAAAAA 1451

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Job time : 379.544 secs

Job time : 379.544 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: December 4, 2005, 20:43:36 : Search time 238.244 Seconds
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Title: US-10-750-262-1

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1195	100.0	1195	3	US-09-323-873A-1 Sequence 1, Appli
2	1195	100.0	1195	3	US-09-685-166A-878 Sequence 878, App
3	1195	100.0	1195	3	US-09-679-426-878 Sequence 878, App
4	1195	100.0	1195	3	US-09-759-143-878 Sequence 878, App
5	1195	100.0	1195	3	US-10-010-667A-1 Sequence 1, Appli
6	1195	100.0	1195	3	US-10-012-896-878 Sequence 878, App
7	1193	99.8	1193	3	US-09-455-486-1 Sequence 1, Appli
8	1143.4	95.7	1147	3	US-09-948-016-2686 Sequence 2686, Ap
9	825.6	69.1	3627	3	US-09-323-873A-6 Sequence 6, Appli
10	825.6	69.1	3627	3	US-09-455-486-4 Sequence 4, Appli
11	825.6	69.1	3627	3	US-10-010-667A-6 Sequence 6, Appli
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13	581	48.6	592	3	US-09-352-616A-342 Sequence 342, App
14	581	48.6	592	3	US-09-636-215-342 Sequence 342, App
15	581	48.6	592	3	US-09-685-166A-342 Sequence 342, App
16	581	48.6	592	3	US-09-679-426-342 Sequence 342, App
17	581	48.6	592	3	US-09-759-143-342 Sequence 342, App
18	581	48.6	592	3	US-09-651-236-342 Sequence 342, App
19	581	48.6	592	3	US-09-657-279-342 Sequence 342, App
20	581	48.6	592	3	US-10-012-896-342 Sequence 342, App
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22	360.6	30.2	455	3	US-09-621-976-9264 Sequence 9264, Ap
23	266.6	22.3	2453	3	US-09-455-486-5 Sequence 5, Appli
24	266.6	22.3	2469	3	US-10-104-047-1185 Sequence 1185, Ap

25	265	22.2	1403	3	US-10-012-896-995 Sequence 995, App
26	229.6	19.2	848	3	US-10-012-896-993 Sequence 993, App
27	221.4	18.5	519	3	US-10-010-667A-7 Sequence 7, Appli
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29	212.8	17.8	2714	3	US-09-562-930-5 Sequence 5, Appli
30	212.8	17.8	3884	3	US-09-562-930-10 Sequence 10, Appli
31	187.4	15.7	4429	3	US-09-455-486-7 Sequence 7, Appli
32	184.8	15.5	1213	3	US-09-083-521-3 Sequence 3, Appli
33	171	14.3	1886	3	US-09-562-930-1 Sequence 1, Appli
34	166.6	13.9	1203	3	US-09-544-618-6 Sequence 6, Appli
35	162.4	13.6	366	3	US-09-030-607-215 Sequence 215, App
36	162.4	13.6	366	3	US-09-439-313-215 Sequence 215, App
37	162.4	13.6	366	3	US-09-352-616A-215 Sequence 215, App
38	162.4	13.6	366	3	US-09-232-149A-215 Sequence 215, App
39	162.4	13.6	366	3	US-09-159-812-215 Sequence 215, App
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41	162.4	13.6	366	3	US-09-685-166A-215 Sequence 215, App
42	162.4	13.6	366	3	US-09-115-453-215 Sequence 215, App
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44	162.4	13.6	366	3	US-09-679-426-215 Sequence 215, App
45	162.4	13.6	366	3	US-09-759-143-215 Sequence 215, App

ALIGNMENTS

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RESULT 1
US-09-323-873A-1
Sequence 1, Application US/09323873A
Patent No. 6329503
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahana Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saitran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323.873A
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-323-873A-1
Query Match          100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 6.6e-301;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 361 CAACTTCCATCAACAAATATTTTATTAATAATCTGATCTGATCAACAAAGCTTTGC 420
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Db 1081 TGTAGAAATTAAGTATTAACACATTTTGTCAATATTAATTAATTTTATCACAACAT 1140
QY 1141 TCAAGTTTGTATTTGTTAATTAATGATTAATCAAGAAAAA 1195
Db 1141 TCAAGTTTGTATTTGTTAATTAATGATTAATCAAGAAAAA 1195

RESULT 2

US-09-685-166A-878
; Sequence 878, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangshun
; APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-685-166A-878

Query Match 100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 6,6e-301; Indels 0; Gaps 0;
Matches 1195; Conservative 0; Mismatches 0;

QY 1 CCGAGACTCAGCGTCAAGCTAAGGCGAAGAGTGGGTGCTGAAGCCATATTTATATAG 60
Db 1 CCGAGACTCAGCGTCAAGCTAAGGCGAAGAGTGGGTGCTGAAGCCATATTTATATAG 60
QY 61 AATTAAATGAAAGCAGAAAAAGACATCAACAAACCAAGAACTTTGAAAAATGAACTTA 120
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RESULT 4

US-09-759-143-878
; Sequence 878, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-878

Query Match 100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 6, 6e-301;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 421 CAATGTTTCCATCACTCTCTTGGCAATGATTTACCTGCAAGTGTGATAGCAATTTG 480
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Db 721 ATGTGCTCTGGGAATGTTGGGATTTGGCAATACCTGGCTGTGCTGATCATCTATTC 780
QY 781 CATCTGTAGTACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGAA 840
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Db 781 CATCTGTAGTACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGAA 840
QY 841 TTGTTCCCTTTACTGCGCACAAATACACGATGATTTTCCCTGGAATAAGTGATG 900
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Db 841 TTGTTCCCTTTACTGCGCACAAATACACGATGATTTTCCCTGGAATAAGTGATG 900
QY 901 AATTAACAAATTTGATATGATATGATACACCTCAACTTTATGATGATCTGTTCTTCCAA 960
|
|
|
Db 901 AATTAACAAATTTGATATGATATGATACACCTCAACTTTATGATGATCTGTTCTTCCAA 960
QY 961 TTGTTCTCTGATATTTAAAGACATATTCCTGCAATGCTTGAAGAAAGATACGA 1020
|
|
|
Db 961 TTGTTCTCTGATATTTAAAGACATATTCCTGCAATGCTTGAAGAAAGATACGA 1020
QY 1021 AGATTAGACATGTTGGGAAGACGTACCAAAATTAACAAACCTGAGATATGTTCCAGT 1080
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|
|
Db 1021 AGATTAGACATGTTGGGAAGACGTACCAAAATTAACAAACCTGAGATATGTTCCAGT 1080
QY 1081 TGATAGATTACCTGTTTACACACATTTTGTTCATATATGATATATTTTATACCAACATT 1140
|
|
|
Db 1081 TGATAGATTACCTGTTTACACACATTTTGTTCATATATGATATATTTTATACCAACATT 1140
QY 1141 TCAAGTTTGTATTTGTTTAAATGAATTAATTCAGAGAAAAA 1195
|
|
|
Db 1141 TCAAGTTTGTATTTGTTTAAATGAATTAATTCAGAGAAAAA 1195

RESULT 5

US-10-010-667A-1
; Sequence 1, Application US/10010667A
; Patent No. 6887975
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leon, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

```

; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 511582001601
; CURRENT APPLICATION NUMBER: US/10/010,667A
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-010-667A-1

Query Match      100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 6,6e-301;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCGAGACTCAGCGTCAAGCTAAGCGGAGAGTGGGCTGGAAGCCATCTATTATATG 60
DB      1 CCGAGACTCAGCGTCAAGCTAAGCGGAGAGTGGGCTGGAAGCCATCTATTATATG 60
QY      61 AATTAATGAGAAAGCAGAAAGACATCAAAACCAAGAACTTTGGAATAAGAGCTTA 120
DB      61 AATTAATGAGAAAGCAGAAAGACATCAAAACCAAGAACTTTGGAATAAGAGCTTA 120
QY      121 GGAGAAATTTAGAGAGAGATTTATTTGATTAAGAGACAGGAGAGACAGCATCTAA 180
DB      121 GGAGAAATTTAGAGAGAGATTTATTTGATTAAGAGACAGGAGAGACAGCATCTAA 180
QY      181 AAAAGACTGCTTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 240
DB      181 AAAAGACTGCTTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 240
QY      241 CAGAACTTCAGACACAGAGAACTTTTCCACAGTGGGACCTTGCATTTAAATAGCTG 300
DB      241 CAGAACTTCAGACACAGAGAACTTTTCCACAGTGGGACCTTGCATTTAAATAGCTG 300
QY      301 CTATTATAGCATCTCTGACTTTTCTTTTCACTCTTCTGAGGAGATTAATTCACCTTTAG 360
DB      301 CTATTATAGCATCTCTGACTTTTCTTTTCACTCTTCTGAGGAGATTAATTCACCTTTAG 360
QY      361 CAACCTCCCATCAACATATTTTATTAATAATTCATCTCTGATCAACAAAGCTTGC 420
DB      361 CAACCTCCCATCAACATATTTTATTAATAATTCATCTCTGATCAACAAAGCTTGC 420
QY      421 CAATGATTTCCATCACTCTCTGGCATTTGATTTGATTTGATTTGATTTGATTTGATTTG 480
DB      421 CAATGATTTCCATCACTCTCTGGCATTTGATTTGATTTGATTTGATTTGATTTGATTTG 480
QY      481 TCCAACTTCATTAATGAGAACCAAGTATTAAGAGTTTCCACATTTGTTGATTAAGTGAATG 540
DB      481 TCCAACTTCATTAATGAGAACCAAGTATTAAGAGTTTCCACATTTGTTGATTAAGTGAATG 540
QY      541 TAAACAAGAAAGAGTTGGGCTTCTCAGTTTCTTTTCTGCTACTGCTGCAATTTATTA 600
DB      541 TAAACAAGAAAGAGTTGGGCTTCTCAGTTTCTTTTCTGCTACTGCTGCAATTTATTA 600
QY      601 GTCCTGTTTCCATTAAGAGAGGATCTACAGATTAAGAGTTTCTTAACTGGGATTAATCAAC 660
DB      601 GTCCTGTTTCCATTAAGAGAGGATCTACAGATTAAGAGTTTCTTAACTGGGATTAATCAAC 660
QY      661 AGGTCCAAACAAATTAAGAGAGTCTGATTTGAGCATGATTTGAGAAATGAGATTT 720
DB      661 AGGTCCAAACAAATTAAGAGAGTCTGATTTGAGCATGATTTGAGAAATGAGATTT 720
QY      721 ATGTCTCTCTGGGAATTTGGGATTTGGCAATCTGGCTCTGTTGGCTGTGACATCTATTC 780
DB      721 ATGTCTCTCTGGGAATTTGGGATTTGGCAATCTGGCTCTGTTGGCTGTGACATCTATTC 780
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QY      781 CATCTGAGTGAAGCTTTGATGATGAGAGAAATTTCACTATATTGAGAGAGCTAGGAA 840
DB      781 CATCTGAGTGAAGCTTTGATGATGAGAGAAATTTCACTATATTGAGAGAGCTAGGAA 840
QY      841 TTGTTTCCCTTCTACTGGGACAAATACAGCATTTGATTTTCTGGAATTAAGTGAATG 900
DB      841 TTGTTTCCCTTCTACTGGGACAAATACAGCATTTGATTTTCTGGAATTAAGTGAATG 900
QY      901 ATATTAACAAATTTGATGATGATTAACAGCTTCACTTTATGATGCTTTTCTTCCAA 960
DB      901 ATATTAACAAATTTGATGATGATTAACAGCTTCACTTTATGATGCTTTTCTTCCAA 960
QY      961 TTGTTTCCCTTCTACTGGGACAAATACAGCATTTGATTTTCTGGAATTAAGTGAATG 1020
DB      961 TTGTTTCCCTTCTACTGGGACAAATACAGCATTTGATTTTCTGGAATTAAGTGAATG 1020
QY      1021 AGATTAAGCATGTTGGGAGAGCGTCACCAAAATTAACAAACCTGAGATATGTTCCAGT 1080
DB      1021 AGATTAAGCATGTTGGGAGAGCGTCACCAAAATTAACAAACCTGAGATATGTTCCAGT 1080
QY      1081 TGTAGAAATTAAGCTTTTACACATTTTGTGATTTGATTTATTTATTCACCAATTT 1140
DB      1081 TGTAGAAATTAAGCTTTTACACATTTTGTGATTTGATTTATTTATTCACCAATTT 1140
QY      1141 TCAAGTTGTTGTTGTTAATAAATGATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1195
DB      1141 TCAAGTTGTTGTTGTTAATAAATGATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1195
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RESULT 6
US-10-012-896-878
; Sequence 878, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vinals de Baseols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Panger, Gary R.
; APPLICANT: Mantabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-012-896-878

Query Match      100.0%; Score 1195; DB 3; Length 1195;
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Best Local Similarity 100.0%; Pred. No. 6,6e-301; Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCGAGACTCAGGTCAGCTAAGCGAAAGTGGTGGCTGAAGCCATCTATTTTATAG 60
Db 1 CCGAGACTCAGGTCAGCTAAGCGAAAGTGGTGGCTGAAGCCATCTATTTTATAG 60
QY 61 AATTAAAGAAAGAGAAAGAAAGATCAAAACCAAGAAAGCTTTGAAATGAAGCTTA 120
Db 61 AATTAAAGAAAGAGAAAGAAAGATCAAAACCAAGAAAGCTTTGAAATGAAGCTTA 120
QY 121 GGAGAAATTTAGAAAGAGAGATTAATTTGATTAAGAGACAGGAGAGACAGCATGTAA 180
Db 121 GGAGAAATTTAGAAAGAGAGATTAATTTGATTAAGAGACAGGAGAGACAGCATGTAA 180
QY 181 AAAGACCTGTCTTTTGAATTTGACCAAGCCCATGCTGAATTTTGAAGCTT 240
Db 181 AAAGACCTGTCTTTTGAATTTGACCAAGCCCATGCTGAATTTTGAAGCTT 240
QY 241 CAGAACTTCAGACACACAGAACTCTTCCAGAGTGCACTTGGCAATTAATAGCTG 300
Db 241 CAGAACTTCAGACACACAGAACTCTTCCAGAGTGCACTTGGCAATTAATAGCTG 300
QY 301 CTATATATAGCATCTCTGACTTTTCTTTA CACTCTTTGAGGGAATTAATCCCTTTAG 360
Db 301 CTATATATAGCATCTCTGACTTTTCTTTA CACTCTTTGAGGGAATTAATCCCTTTAG 360
QY 361 CAATCTCCATCAACAATTTTATTAATTAATTCATCTGCTCATCAAGAAAGCTTGC 420
Db 361 CAATCTCCATCAACAATTTTATTAATTAATTCATCTGCTCATCAAGAAAGCTTGC 420
QY 421 CAATGTTTCCATCACTCTCTTGGCAATTTTCACTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 CAATGTTTCCATCACTCTCTTGGCAATTTTCACTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 TCCAACTTCATTAATGAACCAAGTAATGAAGTTTCCAGTTGTTGATTAAGTGAAT 540
Db 481 TCCAACTTCATTAATGAACCAAGTAATGAAGTTTCCAGTTGTTGATTAAGTGAAT 540
QY 541 TAAAGAAAGAGAGTTGGGCTTCTCAGTTTCTTTTGGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 TAAAGAAAGAGAGTTGGGCTTCTCAGTTTCTTTTGGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 GTCTGTCTTACCAATGAGGCGATCTCAGATACAGATTAAGTTGCTGCTGCTGCTGCTG 660
Db 601 GTCTGTCTTACCAATGAGGCGATCTCAGATACAGATTAAGTTGCTGCTGCTGCTGCTG 660
QY 661 AGGTCCAACAAATTAAGAAAGATGCTGATTAAGATGATTTGGAATGGAATTT 720
Db 661 AGGTCCAACAAATTAAGAAAGATGCTGATTAAGATGATTTGGAATGGAATTT 720
QY 721 ATGTGTCTCTGGGAATTTGGGATTTGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 ATGTGTCTCTGGGAATTTGGGATTTGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 CATCTGTGAGTACTCTTTGACATGAGAGAAATTTCACTATATTGAGAGAACTGAGAA 840
Db 781 CATCTGTGAGTACTCTTTGACATGAGAGAAATTTCACTATATTGAGAGAACTGAGAA 840
QY 841 TTGTTTCCCTTCTTACCTGGGCAATACAGCATTTGATTTTGGCTGGAATTAAGTGAATG 900
Db 841 TTGTTTCCCTTCTTACCTGGGCAATACAGCATTTGATTTTGGCTGGAATTAAGTGAATG 900
QY 901 AATTAATAACAATTTGATGATTAACACTTCCAACTTTTATGATAGCTGTTTCTTCCAA 960
Db 901 AATTAATAACAATTTGATGATTAACACTTCCAACTTTTATGATAGCTGTTTCTTCCAA 960
QY 961 TTGTTTCCCTGATTAATTAAGCATACTATTTCCGCACTGCTGAGGAAAGAAATGCTGA 1020
Db 961 TTGTTTCCCTGATTAATTAAGCATACTATTTCCGCACTGCTGAGGAAAGAAATGCTGA 1020
QY 1021 AGATTAGACATGTTGGGAAGAGCTCAAAAATTAACAAACTGAGATATGTTCCAGT 1080
Db 1021 AGATTAGACATGTTGGGAAGAGCTCAAAAATTAACAAACTGAGATATGTTCCAGT 1080
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Db 1021 AGATTAGACATGTTGGGAAGAGCTCAAAAATTAACAAACTGAGATATGTTCCAGT 1080
QY 1081 TGTAGATTAATCTGTTTACACACATTTTGTCAATATGATATTTATTCACCAACTT 1140
Db 1081 TGTAGATTAATCTGTTTACACACATTTTGTCAATATGATATTTATTCACCAACTT 1140
QY 1141 TCAAGTTTGTATTTGTTTATTAATTAATGATTTTCAAGGAAAAAAGAAAAA 1195
Db 1141 TCAAGTTTGTATTTGTTTATTAATTAATGATTTTCAAGGAAAAAAGAAAAA 1195
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RESULT 7

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US-09-455-486-1
; Sequence 1, Application US/09455486
; Patent No. 6833438
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USBS THEROOF
; FILE REFERENCE: 129.17-US-11
; CURRENT APPLICATION NUMBER: US/09/455.486
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/323.873
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)
US-09-455-486-1
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Query Match 99.8%; Score 1193; DB 3; Length 1193;
Best Local Similarity 100.0%; Pred. No. 2,2e-300; Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 GAGACTCAGGTCAGCTAAGCGAAAGTGGTGGCTGAAGCCATCTATTTTATAGAA 62
Db 1 GAGACTCAGGTCAGCTAAGCGAAAGTGGTGGCTGAAGCCATCTATTTTATAGAA 60
QY 63 TTAATGGAAGAGAAAGAGATCAACAACCAAGAAAGCTTTGAAATGAAGCTTAGG 122
Db 61 TTAATGGAAGAGAAAGAGATCAACAACCAAGAAAGCTTTGAAATGAAGCTTAGG 120
QY 123 AGAAATTTAGAAAGAGAGATTAATTTGATTAAGAGACAGGAGAGACAGCATGCTAAA 182
Db 121 AGAAATTTAGAAAGAGAGATTAATTTGATTAAGAGACAGGAGAGACAGCATGCTAAA 180
QY 183 AGACCTGTGCTTTTGGATTTGGACCAACAGCCCATGCTGAATTTGACTGCTTCA 242
Db 181 AGACCTGTGCTTTTGGATTTGGACCAACAGCCCATGCTGAATTTGACTGCTTCA 240
QY 243 GAACCTTGAGCACACAGGAAGCTTTTCCAGAGTGGCACTTGCATTAATTAATAGCTGCT 302
Db 241 GAACCTTGAGCACACAGGAAGCTTTTCCAGAGTGGCACTTGCATTAATTAATAGCTGCT 300
QY 303 AATTATAGCATCTGACTTTTCTTTTACACTCTTTGAGGGAATTAATACCTTTAGCA 362
Db 301 AATTATAGCATCTGACTTTTCTTTTACACTCTTTGAGGGAATTAATACCTTTAGCA 360
QY 363 ACTTCCATCAACAATATTTTATTAATTTCCAAATCCGCTGATCAAGAAAGCTTGGCA 422
Db 361 ACTTCCATCAACAATATTTTATTAATTTCCAAATCCGCTGATCAAGAAAGCTTGGCA 420
QY 423 ATGGTTTCATCACTCTTGGCAATTTGTTTACTGCTGCTGCTGCTGCTGCTGCTGCTG 482
Db 423 ATGGTTTCATCACTCTTGGCAATTTGTTTACTGCTGCTGCTGCTGCTGCTGCTGCTG 482
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Db 421 ATGGTTCATCACTCTTGGCAGTTGGTTTACCTGCGAGGTGTAGACGAATTTGTC 480
Qy 483 CAACCTCATATGGAACCAAGTATAGAAAGTTTCCACATTTGGTGAATAGTGAATGTTA 542
Db 481 CAACCTCATATGGAACCAAGTATAGAAAGTTTCCACATTTGGTGAATAGTGAATGTTA 540
Qy 543 ACAAGAAAGAGTTGGGCTTCTGAGTTTCTTTTCTGTAATGCAATGCAATTTTATAGT 602
Db 541 ACAAGAAAGAGTTGGGCTTCTGAGTTTCTTTTCTGTAATGCAATGCAATTTTATAGT 600
Qy 603 CTGTCTTACCCCAATGAGGCGATCTTACAGATACAAAGTTGCTAAATCGGCGATATCAACAG 662
Db 601 CTGTCTTACCCCAATGAGGCGATCTTACAGATACAAAGTTGCTAAATCGGCGATATCAACAG 660
Qy 663 GTCACCAAAATATAAGAAAGATGCTGTGATGAGCATGATGTTGGAGATGAGATTTAT 722
Db 661 GTCACCAAAATATAAGAAAGATGCTGTGATGAGCATGATGTTGGAGATGAGATTTAT 720
Qy 723 GTGTCTCTGGAAATTTGGGATTTGGCAATACTGGCTCTGTGGCTGTGATCATTTTCCA 782
Db 721 GTGTCTCTGGAAATTTGGGATTTGGCAATACTGGCTCTGTGGCTGTGATCATTTTCCA 780
Qy 783 TCTGTAGTACCTCTTTGACATGAGAGAAATTTTCACTATATTCAGAGCAAGCTAGGAAAT 842
Db 781 TCTGTAGTACCTCTTTGACATGAGAGAAATTTTCACTATATTCAGAGCAAGCTAGGAAAT 840
Qy 843 GTTTCCTCTACTGGGCAATATACAGCATGATTTTGGCTGGAAATAGTGATGAT 902
Db 841 GTTTCCTCTACTGGGCAATATACAGCATGATTTTGGCTGGAAATAGTGATGAT 900
Qy 903 ATAAACAATTTGTATGATATACACCTCAACTTTTATGATAGCTGTTTCTTCCAAAT 962
Db 901 ATAAACAATTTGTATGATATACACCTCAACTTTTATGATAGCTGTTTCTTCCAAAT 960
Qy 963 GTTTCCTCTATTTAAAGCATATCTTCTGCGCATGCTTGAAGAAAGATATCTGAAG 1022
Db 961 GTTTCCTCTATTTAAAGCATATCTTCTGCGCATGCTTGAAGAAAGATATCTGAAG 1020
Qy 1023 ATTAGCATGTGGGAGAGCGTCAACAAATTAACAAACCTGAGATGTTCCCGATG 1082
Db 1021 ATTAGCATGTGGGAGAGCGTCAACAAATTAACAAACCTGAGATGTTCCCGATG 1080
Qy 1083 TAGAATTAATCTTTTACACATTTTGTTCATATTTATTTTATACCAACATTTTC 1142
Db 1081 TAGAATTAATCTTTTACACATTTTGTTCATATTTATTTTATACCAACATTTTC 1140
Qy 1143 AAGTTGTAATTTGTAATAAATGATTTATTCAGAGAAAAAATTTTAAAAA 1195
Db 1141 AAGTTGTAATTTGTAATAAATGATTTATTCAGAGAAAAAATTTTAAAAA 1193

RESULT 8
US-09-949-016-2686
; Sequence 2686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2686
; LENGTH: 1147
; TYPE: DNA

; ORGANISM: Human
US-09-949-016-2686
Query Match 95.7%; Score 1143.4; DB 3; Length 1147;
Best Local Similarity 99.9%; Pred. No. 1.7e-287;
Matches 1144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 34 GTGGCTGAAGCCATATATTTATGAAATTAATGAAAGACAGAAAGACATCAAAACC 93
Db 1 GTGGCTGAAGCCATATATTTATGAAATTAATGAAAGACAGAAAGACATCAAAACC 60
Qy 94 AAGAAGACTTTGAAAAATGAAGCCTTAGAGAAATTTAGAAAGACGATTAATTTGCATA 153
Db 61 AAGAAGACTTTGAAAAATGAAGCCTTAGAGAAATTTAGAAAGACGATTAATTTGCATA 120
Qy 154 AGGACACGGGAGAGACAGACATGCTAAAAAGACCTGTGCTTTTGGCATTTGACCAACAG 213
Db 121 AGGACACGGGAGAGACAGACATGCTAAAAAGACCTGTGCTTTTGGCATTTGACCAACAG 180
Qy 214 CCATGCTGATGAAATTTGACTGCTTCAAGAACTTGACAGACACAGAACTCTTTCAC 273
Db 181 CCATGCTGATGAAATTTGACTGCTTCAAGAACTTGACAGACACAGAACTCTTTCAC 240
Qy 274 AGTGCACTTGGCCCAATTAATAGCTGCTAATTAATGACATCTGACTTTTCTTTACATC 333
Db 241 AGTGCACTTGGCCCAATTAATAGCTGCTAATTAATGACATCTGACTTTTCTTTACATC 300
Qy 334 TTCTGAGGAGATTAATTCACCTTTTACAACTTCCATCAACATATTTTATTAATTC 393
Db 301 TTCTGAGGAGATTAATTCACCTTTTACAACTTCCATCAACATATTTTATTAATTC 360
Qy 394 CAATCTGGATCAACAAAGTCTTGGCAATGTTTCCATGCTCTTGGCATGTTGTT 453
Db 361 CAATCTGGATCAACAAAGTCTTGGCAATGTTTCCATGCTCTTGGCATGTTGTT 420
Qy 454 ACCTCGAGGTGATAGAGCAATTTGTCCAACTTCTAATATGAAACCAAGTATMAAGAT 513
Db 421 ACCTCGAGGTGATAGAGCAATTTGTCCAACTTCTAATATGAAACCAAGTATMAAGAT 480
Qy 514 TTTCACATTTGTTGATTAAGTGTTAACAAGAAAGCAATTTGGGCTTCTGAGTTTCT 573
Db 481 TTTCACATTTGTTGATTAAGTGTTAACAAGAAAGCAATTTGGGCTTCTGAGTTTCT 540
Qy 574 TTTTGTCTGATGCAATGCAATTTTATGCTGCTTACCATGAGGCGATCCTACAGAT 633
Db 541 TTTTGTCTGATGCAATGCAATTTTATGCTGCTTACCATGAGGCGATCCTACAGAT 600
Qy 634 ACAAGTTGCTAAACTGGGCATATCAACAGGTCCAAACAAATTAAGAAAGATGCTGATG 693
Db 601 ACAAGTTGCTAAACTGGGCATATCAACAGGTCCAAACAAATTAAGAAAGATGCTGATG 660
Qy 694 AGCATGATTTTGGAGATGAGAGATTTATGCTCTGCGGAATTTGGAGTTGGCAATAC 753
Db 661 AGCATGATTTTGGAGATGAGAGATTTATGCTCTGCGGAATTTGGAGTTGGCAATAC 720
Qy 754 TGGCTCTGTGGCTGAGATCATTTTCCATCTGTGAGTACCTTTGATGAGAGAT 813
Db 721 TGGCTCTGTGGCTGAGATCATTTTCCATCTGTGAGTACCTTTGATGAGAGAT 780
Qy 814 TTCACTATATTCAGAGCAAGTAGAATTTTCCCTTCTACTGCGGCAACATACAGCAT 873
Db 781 TTCACTATATTCAGAGCAAGTAGAATTTTCCCTTCTACTGCGGCAACATACAGCAT 840
Qy 874 TGATTTTGGCTGGAATTAAGTGAATATTAACAAATTTGATGATATACACTTCCAA 933
Db 841 TGATTTTGGCTGGAATTAAGTGAATATTAACAAATTTGATGATATACACTTCCAA 900
Qy 934 CTTTATGATACCTTTTCTTCAATTTGTTGCTGATATTTTAAAGCATACTATTC 993
Db 901 CTTTATGATACCTTTTCTTCAATTTGTTGCTGATATTTTAAAGCATACTATTC 960
Qy 994 TCCCATGCTTGAAGAAAGATATGAAATTTAGACATGTTTGGAGAGCGTACCAAAA 1053

Db 961 TGCCATGCTTGAGAGAGAACTAGAAATTTAGACATGTTGGAGACGTCACCAAAA 1020
Qy 1054 TTAACAAAAGTGAATATGTTCCAGTTGTAGAAATTTACTGTTTACACATTTTGTTC 1113
Db 1021 TTAACAAAAGTGAATATGTTCCAGTTGTAGAAATTTACTGTTTACACATTTTGTTC 1080
Qy 1114 ATATTGATATATTTTATGACCAACATTTCAAGTTGTATTTGTTATATAAATGATATTC 1173
Db 1081 ATATTGATATATTTTATGACCAACATTTCAAGTTGTATTTGTTATATAAATGATATTC 1140
Qy 1174 AAGGA 1178
Db 1141 AAGGA 1145

RESULT 9
US-09-323-873A-6
Sequence 6, Application US/09323873A
Patent No. 6329503
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 3627
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-323-873A-6

Query Match 69.1%; Score 825.6; DB 3; Length 3627;
Best Local Similarity 99.5%; Pred. No. 1.2e-204;
Matches 828; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CCGAGACTACGGTCAAGCTTAAGGCGAAGAGTGGTGGCTGAAGCCATATTTATAG 60
Db 31 CCGAGACTACGGTCAAGCTTAAGGCGAAGAGTGGTGGCTGAAGCCATATTTATAG 90
Qy 61 AATTATGGAAGCAGAAAAGCATCAAAACCAAGAAAGCTTTGGAATAAGAGCTTA 120
Db 91 AATTATGGAAGCAGAAAAGCATCAAAACCAAGAAAGCTTTGGAATAAGAGCTTA 150
Qy 121 GGAGAAATTTAGAGAGAGCATTTATTTGATTAAGACACGGAGAGACCAAGATGCTAA 180
Db 151 GGAGAAATTTAGAGAGAGCATTTATTTGATTAAGACACGGAGAGACCAAGATGCTAA 210
Qy 181 AAGAGCTGTGCTTTTGGCATTTGGACCAAAACAGCCCATCTGATGTAATTTGACTGCCCT 240
Db 211 AAGAGCTGTGCTTTTGGCATTTGGACCAAAACAGCCCATCTGATGTAATTTGACTGCCCT 270
Qy 241 CAGAACTTGAGCAGACAGAAAGCTTTTCCACAGTGGACCTTGCCAAATTAATAATAGCTG 300
Db 271 CAGAACTTGAGCAGACAGAAAGCTTTTCCACAGTGGACCTTGCCAAATTAATAATAGCTG 330
Qy 301 CTATTATAGCATCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATTACCCCTTTAG 360
Db 331 CTATTATAGCATCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATTACCCCTTTAG 390
Qy 361 CAATCTCCATCAACAATATTTTATTAATAATTTCCATCTGTCATCAACAAGCTTTCG 420

Db 391 CAATCTCCATCAACAATATTTTATTAATAATTTCCATCTGTCATCAACAAGCTTTCG 450
Qy 421 CAATGTTTTCATCACTCTCTTGCAATTTGTTTACCTGCGCAGGTGTATAGCACAATTTG 480
Db 451 CAATGTTTTCATCACTCTCTTGCAATTTGTTTACCTGCGCAGGTGTATAGCACAATTTG 510
Qy 481 TCCAACTTCAATAAGGAAGCAGATTAAGAAAGTTTCCACATTTGTTGGAATAGTGTGT 540
Db 511 TCCAACTTCAATAAGGAAGCAGATTAAGAAAGTTTCCACATTTGTTGGAATAGTGTGT 570
Qy 541 TAAACAGAAAGCAGTTTGGGCTTCTCAAGTTTCTTTTGTCTGTACTGCATCAATTTATA 600
Db 571 TAAACAGAAAGCAGTTTGGGCTTCTCAAGTTTCTTTTGTCTGTACTGCATCAATTTATA 630
Qy 601 GTCTGTTTACCATAAGGCGATCTTACATACAACTTCTAACTGGCCATATGAC 660
Db 631 GTCTGTTTACCATAAGGCGATCTTACATACAACTTCTAACTGGCCATATGAC 690
Qy 661 AGGTCCAAACAATAAAGAAAGATGCTGGATTTGACATGATGTTTGGAGATGAGATTT 720
Db 691 AGGTCCAAACAATAAAGAAAGATGCTGGATTTGACATGATGTTTGGAGATGAGATTT 750
Qy 721 ATGTCTCTGGAATTTGGGATTTGGCAATAGCTGCTGTTGGCTGTGACATCTATTC 780
Db 751 ATGTCTCTGGAATTTGGGATTTGGCAATAGCTGCTGTTGGCTGTGACATCTATTC 810
Qy 781 CATCTGTGAGTACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCA 832
Db 811 CATCTGTGAGTACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGTAA 862

RESULT 10
US-09-455-486-4
Sequence 4, Application US/09455486
Patent No. 6833438
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.17-US-11
CURRENT APPLICATION NUMBER: US/09/455,486
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 3627
TYPE: DNA
ORGANISM: Homo sapiens
US-09-455-486-4

Query Match 69.1%; Score 825.6; DB 3; Length 3627;
Best Local Similarity 99.5%; Pred. No. 1.2e-204;
Matches 828; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CCGAGACTACGGTCAAGCTTAAGGCGAAGAGTGGTGGCTGAAGCCATATTTATAG 60
Db 31 CCGAGACTACGGTCAAGCTTAAGGCGAAGAGTGGTGGCTGAAGCCATATTTATAG 90
Qy 61 AATTATGGAAGCAGAAAAGCATCAAAACCAAGAAAGCTTTGGAATAAGAGCTTA 120
Db 91 AATTATGGAAGCAGAAAAGCATCAAAACCAAGAAAGCTTTGGAATAAGAGCTTA 150
Qy 121 GGAGAAATTTAGAGAGAGCATTTATTTGATTAAGACACGGAGAGACCAAGATGCTAA 180
Db 151 GGAGAAATTTAGAGAGAGCATTTATTTGATTAAGACACGGAGAGACCAAGATGCTAA 210
Qy 181 AAGAGCTGTGCTTTTGGCATTTGGACCAAAACAGCCCATCTGATGTAATTTGACTGCCCT 240

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Db 211 AAGACCTGCTTTTCATTTGACCAACAGCCCATGCGAATGGAATTTGACCTGCTT 270
Qy 241 CAGAACTTGCACACACAGGAACCTTTTCCAGAGTGGCACTTGGCAATTAATAGCTG 300
Db 271 CAGAACTTGCACACACAGGAACCTTTTCCAGAGTGGCACTTGGCAATTAATAGCTG 330
Qy 301 CTATTATAGCATCTCTGACTTTCTTTTCACTCTTCTGAGGAGATTAATCACTTCTTAC 360
Db 331 CTATTATAGCATCTCTGACTTTCTTTTCACTCTTCTGAGGAGATTAATCACTTCTTAC 390
Qy 361 CAACCTTCCATCAACAATATTTTATATAAATTCATCTGCTGATCAACAAGCTTTGC 420
Db 391 CAACCTTCCATCAACAATATTTTATATAAATTCATCTGCTGATCAACAAGCTTTGC 450
Qy 421 CAATGTTTCCATCACTCTCTGCGCATTTGTTTACCTGCGACAGGTGATGCGCAATTC 480
Db 451 CAATGTTTCCATCACTCTCTGCGCATTTGTTTACCTGCGACAGGTGATGCGCAATTC 510
Qy 481 TCCAACTTCAATAAGAACCAAGATATAGAAAGTTTCCAACTGTTGATTAAGTGAATG 540
Db 511 TCCAACTTCAATAAGAACCAAGATATAGAAAGTTTCCAACTGTTGATTAAGTGAATG 570
Qy 541 TAAACAAGAAAGCAGTTGGGCTTCTCACTTTCTTTTCTGCTGATCTGATGCAATTTAA 600
Db 571 TAAACAAGAAAGCAGTTGGGCTTCTCACTTTCTTTTCTGCTGATCTGATGCAATTTAA 630
Qy 601 GTCTGCTTACCAATGAGGCGATCTTACAGATACAAAGTGTAAATCTGGGCAATTAAC 660
Db 631 GTCTGCTTACCAATGAGGCGATCTTACAGATACAAAGTGTAAATCTGGGCAATTAAC 690
Qy 661 AGGTCCAAACAAATAAAGAAATGCTGATGAGTGAATGATGTTGGAGATGAGATTT 720
Db 691 AGGTCCAAACAAATAAAGAAATGCTGATGAGTGAATGATGTTGGAGATGAGATTT 750
Qy 721 ATGTGCTCTGGAAATTTGGGAATGGCAATCTGCTGTTGGCTGATCAATCTAATTC 780
Db 751 ATGTGCTCTGGAAATTTGGGAATGGCAATCTGCTGTTGGCTGATCAATCTAATTC 810
Qy 781 CATCTGTAGTGAATCTTTGACATGAGAGAAATTTCACTAATTTCAAGTAA 832
Db 811 CATCTGTAGTGAATCTTTGACATGAGAGAAATTTCACTAATTTCAAGTAA 862

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RESULT 11

US-10-010-667A-6
Sequence 6, Application US/10010667A

Patent No. 6887975
GENERAL INFORMATION:

APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arthur B.
APPLICANT: Saitran, Douglas C.
APPLICANT: Mitchell, Steve Serpentine
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
FILE REFERENCE: 511582001601
CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6
LENGTH: 3627
TYPE: DNA
ORGANISM: Homo sapiens
US-10-010-667A-6

Query Match 69.1%; Score 825.6; DB 3; Length 3627;
Best Local Similarity 99.5%; Pred. No. 1.2e-204;
Matches 828; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 CCGAGACTCAGCGTCAAGCTTAAGCGCAAGAGTGGTGGCTGAAGCCATATATTTATAG 60
Db 31 CCGAGACTCAGCGTCAAGCTTAAGCGCAAGAGTGGTGGCTGAAGCCATATATTTATAG 90
Qy 61 AATTAATGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 120
Db 91 AATTAATGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 150
Qy 121 GGAGAAATTTAGAAAGAGAGATTAATTTGATTAAGAGACCGGAGAGACAGCATGCTAA 180
Db 151 GGAGAAATTTAGAAAGAGAGATTAATTTGATTAAGAGACCGGAGAGACAGCATGCTAA 210
Qy 181 AAGACCTGCTTTTTCATTTGATGACCAACAGCCCATGCTGATGAATTTGACTGCTT 240
Db 211 AAGACCTGCTTTTTCATTTGATGACCAACAGCCCATGCTGATGAATTTGACTGCTT 270
Qy 241 CAGAACTTCAAGCAACACAGGAATCTTTTCCAGAGTGGCACTTGGCAATTAATAGCTG 300
Db 271 CAGAACTTCAAGCAACACAGGAATCTTTTCCAGAGTGGCACTTGGCAATTAATAGCTG 330
Qy 301 CTATTATAGCATCTCTGACTTTCTTTTCACTCTTCTGAGGAGATTAATCACTTCTTAC 360
Db 331 CTATTATAGCATCTCTGACTTTCTTTTCACTCTTCTGAGGAGATTAATCACTTCTTAC 390
Qy 361 CAACCTTCCATCAACAATATTTTATATAAATTCATCTGCTGATCAACAAGCTTTGC 420
Db 391 CAACCTTCCATCAACAATATTTTATATAAATTCATCTGCTGATCAACAAGCTTTGC 450
Qy 421 CAATGTTTCCATCACTCTCTGCGCATTTGTTTACCTGCGACAGGTGATGCGCAATTC 480
Db 451 CAATGTTTCCATCACTCTCTGCGCATTTGTTTACCTGCGACAGGTGATGCGCAATTC 510
Qy 481 TCCAACTTCAATAAGAACCAAGATATAGAAAGTTTCCAACTGTTGATTAAGTGAATG 540
Db 511 TCCAACTTCAATAAGAACCAAGATATAGAAAGTTTCCAACTGTTGATTAAGTGAATG 570
Qy 541 TAAACAAGAAAGCAGTTGGGCTTCTCACTTTCTTTTCTGCTGATCTGATGCAATTTAA 600
Db 571 TAAACAAGAAAGCAGTTGGGCTTCTCACTTTCTTTTCTGCTGATCTGATGCAATTTAA 630
Qy 601 GTCTGCTTACCAATGAGGCGATCTTACAGATACAAAGTGTAAATCTGGGCAATTAAC 660
Db 631 GTCTGCTTACCAATGAGGCGATCTTACAGATACAAAGTGTAAATCTGGGCAATTAAC 690
Qy 661 AGGTCCAAACAAATAAAGAAATGCTGATGAGTGAATGATGTTGGAGATGAGATTT 720
Db 691 AGGTCCAAACAAATAAAGAAATGCTGATGAGTGAATGATGTTGGAGATGAGATTT 750
Qy 721 ATGTGCTCTGGAAATTTGGGAATGGCAATCTGCTGTTGGCTGATCAATCTAATTC 780
Db 751 ATGTGCTCTGGAAATTTGGGAATGGCAATCTGCTGTTGGCTGATCAATCTAATTC 810
Qy 781 CATCTGTAGTGAATCTTTGACATGAGAGAAATTTCACTAATTTCAAGTAA 832
Db 811 CATCTGTAGTGAATCTTTGACATGAGAGAAATTTCACTAATTTCAAGTAA 862

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RESULT 12

US-09-439-313-342/C

Sequence 342, Application US/09439313

Patent No. 6329505
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Uiang Yugu
APPLICANT: Reed, Steven G.

APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-342

Query Match 48.6%; Score 581; DB 3; Length 592;
Best Local Similarity 99.7%; Pred. No. 2,6e-141;
Matches 581; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 CCGAGACTCAGGTCAGCTAAGGGAAGTGGGTGCTGAAGCCATCTATTATTATG 60
583 CCGAGACTCAGGTCAGCTAAGGGAAGTGGGTGCTGAAGCCATCTATTATTATG 524
61 AATTATGGAAGCAGAAAGACATCAAAACCAAGAACTTTGAAATGAAGCTTA 120
523 AATTATGGAAGCAGAAAGACATCAAAACCAAGAACTTTGAAATGAAGCTTA 464
121 GGAGAAATTTAGAGAAAGACATTTATTTGATTAAGACACGGAGAGACAGCATGCTTA 180
463 GGAGAAATTTAGAGAAAGACATTTATTTGATTAAGACACGGAGAGACAGCATGCTTA 404
181 AAAGACCTGTGCTTTTGCACTTTTGCAACCAAGCCATGCTGATTAAGTCTGCTT 240
403 AAAGACCTGTGCTTTTGCACTTTTGCAACCAAGCCATGCTGATTAAGTCTGCTT 344
241 CAGAACTTCAGACACACAGAACTCTTTCACAGTGGCACTTGCATTAATAATAGCTG 300
343 CAGAACTTCAGACACACAGAACTCTTTCACAGTGGCACTTGCATTAATAATAGCTG 284
301 CTATTATAGCATCTCTGACTTTTCTTTTACATCTCTTGAAGGAAGTAATTCACCTTTAG 360
283 CTATTATAGCATCTCTGACTTTTCTTTTACATCTCTTGAAGGAAGTAATTCACCTTTAG 224
361 CAACTTCCCATCAACATATTTTATTAATAATCCATCTGTCATCAACAAAGTCTTG 420
223 CAACTTCCCATCAACATATTTTATTAATAATCCATCTGTCATCAACAAAGTCTTG 164
421 CAATGTTTCCATCACTCTCTTGGCATTTGGTTTACCTGCAGGTGTGATAGCAGCAATTG 480
163 CAATGTTTCCATCACTCTCTTGGCATTTGGTTTACCTGCAGGTGTGATAGCAGCAATTG 104
481 TCCAACTTCATTAATGAAGCAAGATTAAGAAAGTTTCCAACTTGGTGAATAGTGATGT 540
103 TCCAACTTCATTAATGAAGCAAGATTAAGAAAGTTTCCAACTTGGTGAATAGTGATGT 44
541 TAAACAAGAAAGCAAGTTGGGCTTCTCAGTTCTTTTGTGCTGT 583
43 TAAACAAGAAAGCAAGTTGGGCTTCTCAGTTCTTTTGTGCTGT 1

RESULT 13
US-09-352-616A-342/C
Sequence 342, Application US/09352616A
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-342

Query Match 48.6%; Score 581; DB 3; Length 592;
Best Local Similarity 99.7%; Pred. No. 2,6e-141;
Matches 581; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 CCGAGACTCAGGTCAGCTAAGGGAAGTGGGTGCTGAAGCCATCTATTATTATG 60
583 CCGAGACTCAGGTCAGCTAAGGGAAGTGGGTGCTGAAGCCATCTATTATTATG 524
61 AATTATGGAAGCAGAAAGACATCAAAACCAAGAACTTTGAAATGAAGCTTA 120
523 AATTATGGAAGCAGAAAGACATCAAAACCAAGAACTTTGAAATGAAGCTTA 464
121 GGAGAAATTTAGAGAAAGACATTTATTTGATTAAGACACGGAGAGACAGCATGCTTA 180
463 GGAGAAATTTAGAGAAAGACATTTATTTGATTAAGACACGGAGAGACAGCATGCTTA 404
181 AAAGACCTGTGCTTTTGCACTTTTGCAACCAAGCCATGCTGATTAAGTCTGCTT 240
403 AAAGACCTGTGCTTTTGCACTTTTGCAACCAAGCCATGCTGATTAAGTCTGCTT 344
241 CAGAACTTCAGACACACAGAACTCTTTCACAGTGGCACTTGCATTAATAATAGCTG 300
343 CAGAACTTCAGACACACAGAACTCTTTCACAGTGGCACTTGCATTAATAATAGCTG 284
301 CTATTATAGCATCTCTGACTTTTCTTTTACATCTCTTGAAGGAAGTAATTCACCTTTAG 360
283 CTATTATAGCATCTCTGACTTTTCTTTTACATCTCTTGAAGGAAGTAATTCACCTTTAG 224
361 CAACTTCCCATCAACATATTTTATTAATAATCCATCTGTCATCAACAAAGTCTTG 420
223 CAACTTCCCATCAACATATTTTATTAATAATCCATCTGTCATCAACAAAGTCTTG 164
421 CAATGTTTCCATCACTCTCTTGGCATTTGGTTTACCTGCAGGTGTGATAGCAGCAATTG 480
163 CAATGTTTCCATCACTCTCTTGGCATTTGGTTTACCTGCAGGTGTGATAGCAGCAATTG 104
481 TCCAACTTCATTAATGAAGCAAGATTAAGAAAGTTTCCAACTTGGTGAATAGTGATGT 540
103 TCCAACTTCATTAATGAAGCAAGATTAAGAAAGTTTCCAACTTGGTGAATAGTGATGT 44
541 TAAACAAGAAAGCAAGTTGGGCTTCTCAGTTCTTTTGTGCTGT 583
43 TAAACAAGAAAGCAAGTTGGGCTTCTCAGTTCTTTTGTGCTGT 1

RESULT 14
US-09-636-215-342/C
Sequence 342, Application US/09636215
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.

```

; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaair A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-342

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Query Match      48.6%; Score 581; DB 3; Length 592;
Best Local Similarity 99.7%; Pred. No. 2,6e-141;
Matches 581; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CCGAGACTCAGGCTCAAGCTTAAGCGGAGAGTGGTGGCTGAAGCCATCTATTATTATAG 60
DB 583 CCGAGACTCAGGCTCAAGCTTAAGCGGAGAGTGGTGGCTGAAGCCATCTATTATTATAG 524
QY 61 AATTATGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 120
DB 523 AATTATGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 464
QY 121 GGAGAATTATGAAGAAGAGATTAATTGCTAAGGACAGGAGAGACAGCATGCTTA 180
DB 463 GGAGAATTATGAAGAAGAGATTAATTGCTAAGGACAGGAGAGACAGCATGCTTA 404
QY 181 AAAGACTGTGCTTTTGCAATTTGCAACCAACAGCCCATGCTGAATTTGACTGCCCTT 240
DB 403 AAAGACTGTGCTTTTGCAATTTGCAACCAACAGCCCATGCTGAATTTGACTGCCCTT 344
QY 241 CAGAACTTCAGCAGCAGCAGGAACTCTTTTCCAGAGTGGCCTTGCCATTTAAATAGCTG 300
DB 343 CAGAACTTCAGCAGCAGCAGGAACTCTTTTCCAGAGTGGCCTTGCCATTTAAATAGCTG 284
QY 301 CTATTATAGCATCTGACTTTCTTTTACACTCTTCTGAGGAGAGTAATTCACCTTTAG 360
DB 283 CTATTATAGCATCTGACTTTCTTTTACACTCTTCTGAGGAGAGTAATTCACCTTTAG 224
QY 361 CAACCTCCATCAACAATATTTTATTAATAATTCATCTGATCATCAACCAAGTCTTG 420
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QY 421 CAATGTTTCCATCACTCTCTTGGCATTTGTTTAACTGCGAGGTGATGACGCAATTG 480
DB 163 CAATGTTTCCATCACTCTCTTGGCATTTGTTTAACTGCGAGGTGATGACGCAATTG 104
QY 481 TCCAACTTCATATGGAACCAAGTATTAAGAGTTTCCATTGCTTGAATTAAGTGAATG 540
DB 103 TCCAACTTCATATGGAACCAAGTATTAAGAGTTTCCATTGCTTGAATTAAGTGAATG 44
QY 541 TAACAAGAAAGCAGTTGGGCTTCTCAGTTCTTTTGGCTGT 583
DB 43 TAACAAGAAAGCAGTTGGGCTTCTCAGTTCTTTTGGCTGT 1

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RESULT 15
US-09-685-166A-342/c
; Sequence 342, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.

```

```

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaair A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-685-166A-342

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Query Match      48.6%; Score 581; DB 3; Length 592;
Best Local Similarity 99.7%; Pred. No. 2,6e-141;
Matches 581; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CCGAGACTCAGGCTCAAGCTTAAGCGGAGAGTGGTGGCTGAAGCCATCTATTATTATAG 60
DB 583 CCGAGACTCAGGCTCAAGCTTAAGCGGAGAGTGGTGGCTGAAGCCATCTATTATTATAG 524
QY 61 AATTATGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 120
DB 523 AATTATGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 464
QY 121 GGAGAATTATGAAGAAGAGATTAATTGCTAAGGACAGGAGAGACAGCATGCTTA 180
DB 463 GGAGAATTATGAAGAAGAGATTAATTGCTAAGGACAGGAGAGACAGCATGCTTA 404
QY 181 AAAGACTGTGCTTTTGCAATTTGCAACCAACAGCCCATGCTGAATTTGACTGCCCTT 240
DB 403 AAAGACTGTGCTTTTGCAATTTGCAACCAACAGCCCATGCTGAATTTGACTGCCCTT 344
QY 241 CAGAACTTCAGCAGCAGCAGGAACTCTTTTCCAGAGTGGCCTTGCCATTTAAATAGCTG 300
DB 343 CAGAACTTCAGCAGCAGCAGGAACTCTTTTCCAGAGTGGCCTTGCCATTTAAATAGCTG 284
QY 301 CTATTATAGCATCTGACTTTCTTTTACACTCTTCTGAGGAGAGTAATTCACCTTTAG 360
DB 283 CTATTATAGCATCTGACTTTCTTTTACACTCTTCTGAGGAGAGTAATTCACCTTTAG 224
QY 361 CAACCTCCATCAACAATATTTTATTAATAATTCATCTGATCATCAACCAAGTCTTG 420
DB 223 CAACCTCCATCAACAATATTTTATTAATAATTCATCTGATCATCAACCAAGTCTTG 164
QY 421 CAATGTTTCCATCACTCTCTTGGCATTTGTTTAACTGCGAGGTGATGACGCAATTG 480
DB 163 CAATGTTTCCATCACTCTCTTGGCATTTGTTTAACTGCGAGGTGATGACGCAATTG 104
QY 481 TCCAACTTCATATGGAACCAAGTATTAAGAGTTTCCATTGCTTGAATTAAGTGAATG 540
DB 103 TCCAACTTCATATGGAACCAAGTATTAAGAGTTTCCATTGCTTGAATTAAGTGAATG 44
QY 541 TAACAAGAAAGCAGTTGGGCTTCTCAGTTCTTTTGGCTGT 583
DB 43 TAACAAGAAAGCAGTTGGGCTTCTCAGTTCTTTTGGCTGT 1

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SUMMARIES

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3	1195	100.0	1195	3	US-09-822-827-878
4	1195	100.0	1195	3	US-09-895-793-878
5	1195	100.0	1195	3	US-09-895-814-878
6	1195	100.0	1195	5	US-10-012-896-878
7	1195	100.0	1195	5	US-10-011-095-1
8	1195	100.0	1195	5	US-10-010-667A-1
9	1195	100.0	1195	5	US-10-205-823-396
10	1195	100.0	1195	6	US-10-144-678A-878
11	1195	100.0	1195	6	US-10-294-025-878
12	1195	100.0	1195	6	US-10-393-590-35
13	1195	100.0	1195	6	US-10-393-567-35
14	1195	100.0	1195	6	US-10-394-087-35
15	1195	100.0	1195	6	US-10-295-027-713
16	1195	100.0	1195	6	US-10-295-027-1130
17	1195	100.0	1195	8	US-10-643-795A-16
18	1195	100.0	1195	8	US-10-643-795A-42
19	1195	100.0	1195	9	US-10-750-262-1
20	1195	100.0	1195	9	US-10-948-518-16
21	1195	100.0	1195	9	US-10-948-518-42
22	1195	100.0	1195	9	US-10-956-157-1811
23	1195	100.0	1195	9	US-10-956-157-7046

24	1195	100.0	1195	9	US-10-858-887-1	Sequence 1, Appli
25	1195	100.0	1195	9	US-10-631-467-428	Sequence 428, App
26	1195	100.0	1195	10	US-11-051-454-396	Sequence 396, App
27	1195	100.0	1330	7	US-10-755-889-191	Sequence 191, App
28	1193	99.8	1193	6	US-10-165-044-1	Sequence 1, Appli
29	1193	99.8	1193	7	US-10-408-009-1	Sequence 1, Appli
30	1193	99.8	1193	8	US-10-857-785-1	Sequence 1, Appli
31	1193	99.8	1193	8	US-10-856-109-1	Sequence 1, Appli
32	1193	99.8	1193	8	US-10-753-195-1	Sequence 1, Appli
33	1193	99.8	1193	8	US-10-752-421-1	Sequence 1, Appli
34	1181.8	98.9	1193	8	US-10-830-899-2	Sequence 2, Appli
35	1181.8	98.9	1193	9	US-10-861-662-2	Sequence 2, Appli
36	1178	98.6	1277	3	US-09-814-353-19910	Sequence 19910, A
37	1177	98.5	1177	8	US-10-696-639-15	Sequence 15, Appli
38	1177	98.5	1201	7	US-10-425-114-16445	Sequence 16445, A
39	1166	97.6	1354	8	US-10-723-860-5120	Sequence 5120, Ap
40	1048	87.7	1365	8	US-10-830-899-6	Sequence 6, Appli
41	1048	87.7	1365	9	US-10-861-662-6	Sequence 6, Appli
42	827.2	69.2	3627	8	US-10-830-899-10	Sequence 10, Appli
43	827.2	69.2	3627	9	US-10-861-662-10	Sequence 10, Appli
44	825.6	69.1	3627	5	US-10-011-095-6	Sequence 6, Appli
45	825.6	69.1	3627	5	US-10-010-667A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-759-143-878
; Sequence 878, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-878

Query Match 100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1.1e+281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGAGCTACGCTCAAGCTAAGCCGAGAGTGGGTGAGCCATACTATTATAG 60
DB 1 CCAGAGCTACGCTCAAGCTAAGCCGAGAGTGGGTGAGCCATACTATTATAG 60

QY 61 AATTAATGGAAGACAGAAAGACATCAAAACCAAGAACTTTGGAAATGAACCTTA 120
DB 61 AATTAATGGAAGACAGAAAGACATCAAAACCAAGAACTTTGGAAATGAACCTTA 120

121 GGAGAAATTAGAGAGAGATTAATTGGATAGAGACAGGGAGAGAGACAGATGCTAA 180
121 GGAGAAATTAGAGAGAGATTAATTGGATAGAGACAGGGAGAGAGACAGATGCTAA 180
181 AAGAGCTGCTGCTTTGGATTTGACACCAACAGCCCATGCTGAATTTGACTGCCCTT 240
181 AAGAGCTGCTGCTTTGGATTTGACACCAACAGCCCATGCTGAATTTGACTGCCCTT 240
241 CAGAACTTGACACACAGAGAACTCTTTCACAGTGGGCACTTGCCCAATTAATACTG 300
241 CAGAACTTGACACACAGAGAACTCTTTCACAGTGGGCACTTGCCCAATTAATACTG 300
301 CTAATTAAGCATCTGACCTTTCTTTTCACTCTTTCAGAGGAAATTAATTCACCTTTAG 360
301 CTAATTAAGCATCTGACCTTTCTTTTCACTCTTTCAGAGGAAATTAATTCACCTTTAG 360
361 CAATCTCCCATCAACATATTTTATTAATAATTCCTGCTGATCAACAAAGCTTTC 420
361 CAATCTCCCATCAACATATTTTATTAATAATTCCTGCTGATCAACAAAGCTTTC 420
421 CAATGTTTCATCACTCTCTTGGCATTTGTTTACCTGCGAGGTGATGACAGCAATTG 480
421 CAATGTTTCATCACTCTCTTGGCATTTGTTTACCTGCGAGGTGATGACAGCAATTG 480
481 TCCAACTTCATATGGAACCAAGTATTAAGAGTTTCCCAATGGTTGATTAAGTGAATG 540
481 TCCAACTTCATATGGAACCAAGTATTAAGAGTTTCCCAATGGTTGATTAAGTGAATG 540
541 TAAACAAGAAAGAGCTTTGGGCTTCTGAGTTCTTTTGTGCTGATCTGACATTTATA 600
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601 GTCTGCTTACCCCAATGAGGCGATCTCAAGATACAAAGTGTAACTGGGCAATCAAC 660
661 AGGTCCAAACAAATTAAGAGATGCTGATGAGATGATGTTGGAGAAATGAGATTT 720
661 AGGTCCAAACAAATTAAGAGATGCTGATGAGATGATGTTGGAGAAATGAGATTT 720
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781 CATCTGAGTGACTCTTTGACATGAGAGAAATTTCACTATTTCAAGAGCACTAGAA 840
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841 TTGTTTCCCTTCTACTGGGCAATACAGCATTTGATTTTGGCTGGAAATTAAGTGAATG 900
901 AATATAAACAATTTGATGATATACACCTCCCACTTTTATGATGATGCTTTTCTTCCCA 960
901 AATATAAACAATTTGATGATATACACCTCCCACTTTTATGATGATGCTTTTCTTCCCA 960
961 TTGTTTCCCTTCTACTGGGCAATACAGCATTTGATTTTGGCTGGAAATTAAGTGAATG 1020
961 TTGTTTCCCTTCTACTGGGCAATACAGCATTTGATTTTGGCTGGAAATTAAGTGAATG 1020
1021 AGATTAGACATGCTGGGAAAGAGCTACCAAAATTAACAAACTGAGATTTGTTCCAGT 1080
1021 AGATTAGACATGCTGGGAAAGAGCTACCAAAATTAACAAACTGAGATTTGTTCCAGT 1080
1081 TGTAGAAATTAAGTATTAACACATTTTGTCAATATGATATATTTTATCACCAACATTT 1140
1081 TGTAGAAATTAAGTATTAACACATTTTGTCAATATGATATATTTTATCACCAACATTT 1140
1141 TCAAGTTTGAATTTGTTAATTAATGATTTTCAAGGAAAAAATTTTAAAAA 1195
1141 TCAAGTTTGAATTTGTTAATTAATGATTTTCAAGGAAAAAATTTTAAAAA 1195

RESULT 2
US-09-780-669-878
; Sequence 878, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuxui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-878
Query Match 100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1,1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CCGAGACTCAGGCTCAGCTTAAGCGGAGAGTGGGTGGCTGAAGCCATATTTATG 60
1 CCGAGACTCAGGCTCAGCTTAAGCGGAGAGTGGGTGGCTGAAGCCATATTTATG 60
61 AATTATGGAAGCGAAGAAAGATCAACAAACCAAGAAAGAACTTGGAAATGAAGCCCTA 120
61 AATTATGGAAGCGAAGAAAGATCAACAAACCAAGAAAGAACTTGGAAATGAAGCCCTA 120
121 GGAGAAATTTAGAGAGAGATTAATTGATTAAGGACACGGGAGAGACAGCATGCTAA 180
121 GGAGAAATTTAGAGAGAGATTAATTGATTAAGGACACGGGAGAGACAGCATGCTAA 180
181 AAGAGCTGCTGCTTTGGATTTGACACCAACAGCCCATGCTGAATTTGACTGCCCTT 240
181 AAGAGCTGCTGCTTTGGATTTGACACCAACAGCCCATGCTGAATTTGACTGCCCTT 240
241 CAGAACTTGACACACAGAGAACTCTTTCACAGTGGGCACTTGCCCAATTAATACTG 300
241 CAGAACTTGACACACAGAGAACTCTTTCACAGTGGGCACTTGCCCAATTAATACTG 300
301 CTAATTAAGCATCTGACCTTTCTTTTCACTCTTTCAGAGGAAATTAATTCACCTTTAG 360
301 CTAATTAAGCATCTGACCTTTCTTTTCACTCTTTCAGAGGAAATTAATTCACCTTTAG 360
361 CAATCTCCCATCAACATATTTTATTAATAATTCCTGCTGATCAACAAAGCTTTC 420
361 CAATCTCCCATCAACATATTTTATTAATAATTCCTGCTGATCAACAAAGCTTTC 420
421 CAATGTTTCATCACTCTCTTGGCATTTGTTTACCTGCGAGGTGATGACAGCAATTG 480
421 CAATGTTTCATCACTCTCTTGGCATTTGTTTACCTGCGAGGTGATGACAGCAATTG 480

Db 421 CAATGTTTCCATCACTCTCTTGGCATTGGTTTACCTCCAGGTGTGATAGCAGCAATTG 480
Qy 481 TCCAACTTCATTAATGGAACCAAGTATTAAGAGTTTCCCATTTGGTGTGATAAGTGAATG 540
Db 481 TCCAACTTCATTAATGGAACCAAGTATTAAGAGTTTCCCATTTGGTGTGATAAGTGAATG 540
Qy 541 TAACAGAAAGCAGTTGGGGCTTCTCAGTTTCTTTTGTCTGTACTGTACATGCAATTTATA 600
Db 541 TAACAGAAAGCAGTTGGGGCTTCTCAGTTTCTTTTGTCTGTACTGTACATGCAATTTATA 600
Qy 601 GTCTGTCTTACCCCAATGAGCGCATCTTACAGTATACAAAGTTGCTAACTGGCGCATTCAC 660
Db 601 GTCTGTCTTACCCCAATGAGCGCATCTTACAGTATACAAAGTTGCTAACTGGCGCATTCAC 660
Qy 661 AGGTCCAAACAAATTAAGAGATGCTGATGAGCATGATGTTTGGAGAAATGAGATTT 720
Db 661 AGGTCCAAACAAATTAAGAGATGCTGATGAGCATGATGTTTGGAGAAATGAGATTT 720
Qy 721 ATGTGTCTCTGGGAATTTGGGAATTTGGCAATACCTGCTCTGTGGCTGTGACATCTATTC 780
Db 721 ATGTGTCTCTGGGAATTTGGGAATTTGGCAATACCTGCTCTGTGGCTGTGACATCTATTC 780
Qy 781 CATCTGTAGTGAATCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTTAGAA 840
Db 781 CATCTGTAGTGAATCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTTAGAA 840
Qy 841 TTGTTTCCCTCTCTCTGGGCAATATACGCAATGATTTTGGCCGTGGAATTAAGTGAATG 900
Db 841 TTGTTTCCCTCTCTCTGGGCAATATACGCAATGATTTTGGCCGTGGAATTAAGTGAATG 900
Qy 901 ATATTAACAAATTTGTATGTATATACCTCCCACTTTTATGATAGCTTTTCTTCCCA 960
Db 901 ATATTAACAAATTTGTATGTATATACCTCCCACTTTTATGATAGCTTTTCTTCCCA 960
Qy 961 TTGTTTCCCTCTCTCTGGGCAATATACGCAATGATTTTGGCCGTGGAATTAAGTGAATG 1020
Db 961 TTGTTTCCCTCTCTCTGGGCAATATACGCAATGATTTTGGCCGTGGAATTAAGTGAATG 1020
Qy 1021 AGATTAGCATGTTGGGAAGCGTACCAAAATTAACAAACTGAGATATGTTCCCACT 1080
Db 1021 AGATTAGCATGTTGGGAAGCGTACCAAAATTAACAAACTGAGATATGTTCCCACT 1080
Qy 1081 TGTGAATTAATCTGTTTACACATTTTGTCAATATGATATATTTTATGACCAACATTT 1140
Db 1081 TGTGAATTAATCTGTTTACACATTTTGTCAATATGATATATTTTATGACCAACATTT 1140
Qy 1141 TCAAGTTTGTATTTGTTATATAATGATTATTCAGAGAAATTTTAAAAATTTTAAAA 1195
Db 1141 TCAAGTTTGTATTTGTTATATAATGATTATTCAGAGAAATTTTAAAAATTTTAAAA 1195

RESULT 3

US-09-822-827-878
; Sequence 878, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: PasteSeq for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-878

Query Match 100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1.le-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGAGACTCAGCGGTCAAGCTTAAGCGAAGAGTGGGTGGCTGAAGCCATTAATTTTATAG 60
Db 1 CCGAGACTCAGCGGTCAAGCTTAAGCGAAGAGTGGGTGGCTGAAGCCATTAATTTTATAG 60
Qy 61 AATTAAATGAAGCAGAAAAAGCATCAACAAACCAAGAACTTTGGAAAAATGAAGCTTA 120
Db 61 AATTAAATGAAGCAGAAAAAGCATCAACAAACCAAGAACTTTGGAAAAATGAAGCTTA 120
Qy 121 GGAGAAATTTTGAAGAAAGCATTAATTTGATATAGGACAGGGAGAAACAGCATGTGTA 180
Db 121 GGAGAAATTTTGAAGAAAGCATTAATTTGATATAGGACAGGGAGAAACAGCATGTGTA 180
Qy 181 AAAGACCTGTGCTTTTGCATTTTGGACCAACAGCCCATGTGTAATTTGACCTT 240
Db 181 AAAGACCTGTGCTTTTGCATTTTGGACCAACAGCCCATGTGTAATTTGACCTT 240
Qy 241 CAGAACTTCAGACACACAGGAACCTTTTCCACAGTGGCACTTGCATTAATTAATAGCTG 300
Db 241 CAGAACTTCAGACACACAGGAACCTTTTCCACAGTGGCACTTGCATTAATTAATAGCTG 300
Qy 301 CTATTATAGCATCTGTGACTTTTCTTTTCACTCTTCTGAGGGAATTAATCACCCTTAG 360
Db 301 CTATTATAGCATCTGTGACTTTTCTTTTCACTCTTCTGAGGGAATTAATCACCCTTAG 360
Qy 361 CAACTTCCCATCAACAAATTTTATTAATAATTCATCTGTGATCAACAAAGCTTTGC 420
Db 361 CAACTTCCCATCAACAAATTTTATTAATAATTCATCTGTGATCAACAAAGCTTTGC 420
Qy 421 CAATGTTTCCATCACTCTCTTGGCATTTGATTAACCTGCAAGTGTATGACAGCAATGG 480
Db 421 CAATGTTTCCATCACTCTCTTGGCATTTGATTAACCTGCAAGTGTATGACAGCAATGG 480
Qy 481 TCCAACTTCATTAATGAACCAAGTAAGAAATTTTCCAACTGTGTGAATGAGT 540
Db 481 TCCAACTTCATTAATGAACCAAGTAAGAAATTTTCCAACTGTGTGAATGAGT 540
Qy 541 TAACAGAAAGCAGTTGGGCTTCTCAGTTTCTTTTGTCTGTACTGATGCAATTTATA 600
Db 541 TAACAGAAAGCAGTTGGGCTTCTCAGTTTCTTTTGTCTGTACTGATGCAATTTATA 600
Qy 601 GTCTGTCTTACCAATGAGCGCATCTTCAAGATTAACAAAGTTGTAACCTGGCGCATTCAC 660
Db 601 GTCTGTCTTACCAATGAGCGCATCTTCAAGATTAACAAAGTTGTAACCTGGCGCATTCAC 660
Qy 661 AGGTCCAAACAAATTAAGAAAGATGCTGATGAGCATGATTTTGGAGAAATGAGATTT 720
Db 661 AGGTCCAAACAAATTAAGAAAGATGCTGATGAGCATGATTTTGGAGAAATGAGATTT 720
Qy 721 ATGTGTCTCTGGGAATTTGGGAATTTGGCAATTAATCTGCTGTGATGATCTATTTC 780
Db 721 ATGTGTCTCTGGGAATTTGGGAATTTGGCAATTAATCTGCTGTGATGATCTATTTC 780
Qy 781 CATCTGTAGTGAATCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTTAGAA 840
Db 781 CATCTGTAGTGAATCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTTAGAA 840
Qy 841 TTGTTTCCCTCTCTCTGGGCAATATACGCAATGATTTTGGCCGTGGAATTAAGTGAATG 900
Db 841 TTGTTTCCCTCTCTCTGGGCAATATACGCAATGATTTTGGCCGTGGAATTAAGTGAATG 900
Qy 901 ATATTAACAAATTTGTATGTATATACCTCCCACTTTTATGATAGCTTTTCTTCCCA 960
Db 901 ATATTAACAAATTTGTATGTATATACCTCCCACTTTTATGATAGCTTTTCTTCCCA 960
Qy 961 TTGTTTCCCTCTCTCTGGGCAATATACGCAATGATTTTGGCCGTGGAATTAAGTGAATG 1020
Db 961 TTGTTTCCCTCTCTCTGGGCAATATACGCAATGATTTTGGCCGTGGAATTAAGTGAATG 1020
Qy 1021 AGATTAGCATGTTGGGAAGCGTACCAAAATTAACAAACTGAGATATGTTCCCACT 1080
Db 1021 AGATTAGCATGTTGGGAAGCGTACCAAAATTAACAAACTGAGATATGTTCCCACT 1080

QY 1081 TGTAGAAATACGTGTTTACACACATTTTGTTCATATTTGATATTTTATCACCACATT 1140
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Db 1081 TGTAGAAATACGTGTTTACACACATTTTGTTCATATTTGATATTTTATCACCACATT 1140
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QY 1141 TCAAGTTGTATTGTTAATAAATGATTTTCAGAGAAAAAATTTTAAAAA 1195
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Db 1141 TCAAGTTGTATTGTTAATAAATGATTTTCAGAGAAAAAATTTTAAAAA 1195

RESULT 4

US-09-895-793-878
; Sequence 878, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hedler, William T.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassoles, Carlota
; APPLICANT: Roy, Teresa
; APPLICANT: Ranger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-878

Query Match 100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1,1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGAGCTCACGCTCAAGCTTAAGCGAAGTGGTGGCTGAAGCCATATTTATATAG 60
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Db 1 CCGAGCTCACGCTCAAGCTTAAGCGAAGTGGTGGCTGAAGCCATATTTATATAG 60
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QY 61 AATTAATGAAAGCAGAAAAAGCATCAAAACCAAGAACTTTGAAAAATGAAGCTTA 120
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QY 121 GGAGAAATTTAGAGAAAGCATTTATTTGCTAAGACACGGAGAGACCATGCTTA 180
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Db 121 GGAGAAATTTAGAGAAAGCATTTATTTGCTAAGACACGGAGAGACCATGCTTA 180
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QY 181 AAAGACTGTGCTTTGCTATTTGCAACCAAGCCCATGTGTATGTAATTTGACTGCCCTT 240
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Db 181 AAAGACTGTGCTTTGCTATTTGCAACCAAGCCCATGTGTATGTAATTTGACTGCCCTT 240
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QY 241 CAGAACTTCAGACACACAGAACTCTTTCCACAGTGGACCTTGCAATTTAAATAGCTG 300
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Db 241 CAGAACTTCAGACACACAGAACTCTTTCCACAGTGGACCTTGCAATTTAAATAGCTG 300

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Db 481 TCCAACTTCAATAAGAACCAAGATTAAGAGTTTCCATGTTGTATAGTGTATG 540
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Db 661 AGGTCCAAACAAATTAAGAAAGATGCTGATTTGAGCATGATGTTGGAAATGAGATT 720
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QY 721 ATGTGCTCTGGGAATGTGGGATTTGGCAATCTGCTGTGTTGGCTGAGACATCTATTC 780
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Db 721 ATGTGCTCTGGGAATGTGGGATTTGGCAATCTGCTGTGTTGGCTGAGACATCTATTC 780
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QY 781 CATCTGTGAGTACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGTATAGAA 840
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Db 781 CATCTGTGAGTACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGTATAGAA 840
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Db 841 TTGTTTCCCTTCTTACTGGGCAATPACGCAATGATTTTCTGCTGGAATTAAGTGATAG 900
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|
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|
Db 901 AATTAATAAATTTGATATGATATACACCTCCAACTTTATGATAGTGTTCCTTCCAA 960
|
|
|
QY 961 TTGTTGCTGCTGATTTTAAAGCATATCTATCTGCGATGCTTGAAGAAAGATPCTGA 1020
|
|
|
Db 961 TTGTTGCTGCTGATTTTAAAGCATATCTATCTGCGATGCTTGAAGAAAGATPCTGA 1020
|
|
|
QY 1021 AGATTAGACATGTTGGGAAAGCTCACCAAAATTAACAAATCTAGATATGTTCCAGT 1080
|
|
|
Db 1021 AGATTAGACATGTTGGGAAAGCTCACCAAAATTAACAAATCTAGATATGTTCCAGT 1080
|
|
|
QY 1081 TGTAGAAATACGTGTTTACACATTTTGTCTCAATATGATATTTATTCACCAACATT 1140
|
|
|
Db 1081 TGTAGAAATACGTGTTTACACATTTTGTCTCAATATGATATTTATTCACCAACATT 1140
|
|
|
QY 1141 TCAAGTTGTATTGTTAATAAATGATTTTCAAGAAAAAATTTTAAAAA 1195
|
|
|
Db 1141 TCAAGTTGTATTGTTAATAAATGATTTTCAAGAAAAAATTTTAAAAA 1195

RESULT 5

US-09-895-814-878
; Sequence 878, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.

```

; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-878

```

```

Query Match      100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1.1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 1 CCGAGACTCAGCGTCAAGCTAAGCGGAGAGTGGGTGGCGGAAGCCATATTTATATG 60
DB 1 CCGAGCTCAGCGTCAAGCTAAGCGGAGAGTGGGTGGCGGAAGCCATATTTATATG 60
QY 61 AATTAATGGAAGCAGAAAAGACATCAAAACCAAGAGAACTTTGGAAAATGAAGCTTA 120
DB 61 AATTAATGGAAGCAGAAAAGACATCAAAACCAAGAGAACTTTGGAAAATGAAGCTTA 120
QY 121 GGAAGAAATTTAGAAAGACGATTTATTTGATTAAGACACGGGAGAGACAGATGCTTA 180
DB 121 GGAAGAAATTTAGAAAGACGATTTATTTGATTAAGACACGGGAGAGACAGATGCTTA 180
QY 181 AAAGACCTGCTGCTTGGCATTTGACCAAAACAGCCCATGCTGTAATTTGACCTGCTT 240
DB 181 AAAGACCTGCTGCTTGGCATTTGACCAAAACAGCCCATGCTGTAATTTGACCTGCTT 240
QY 241 CAGAACTTGAGCAGACAGAAAGCTTTTCCACAGTGGCACTTGCATTTAAATAGCTG 300
DB 241 CAGAACTTGAGCAGACAGAAAGCTTTTCCACAGTGGCACTTGCATTTAAATAGCTG 300
QY 301 CTATTATAGCATCTGACTTTTCTTTTACACTCTTTCTGAGGGAAGTAATTCACCTTTAG 360
DB 301 CTATTATAGCATCTGACTTTTCTTTTACACTCTTTCTGAGGGAAGTAATTCACCTTTAG 360
QY 361 CAATCTCCCATCAAAATATTTTATTAATTTCCATCTCTGCTCAATCAAAAGCTTTGCG 420
DB 361 CAATCTCCCATCAAAATATTTTATTAATTTCCATCTCTGCTCAATCAAAAGCTTTGCG 420
QY 421 CAATGTTTTCATCACTCTCTTGGCATTTGCTTACCTGCGAGGTGATAGCAGAAATG 480
DB 421 CAATGTTTTCATCACTCTCTTGGCATTTGCTTACCTGCGAGGTGATAGCAGAAATG 480
QY 481 TCCAACTTCAATATGGAACCAAGTATTAAGAAAGTTTCCAACTTGGATAGTGATGT 540
DB 481 TCCAACTTCAATATGGAACCAAGTATTAAGAAAGTTTCCAACTTGGATAGTGATGT 540
QY 541 TAACAAAGAAAGAGTTGGGCTTCTAGTTTCTTTTCTGCTGACTGACGCAATTTATA 600
DB 541 TAACAAAGAAAGAGTTGGGCTTCTAGTTTCTTTTCTGCTGACTGACGCAATTTATA 600
QY 601 GTCTGCTTACCAATGAGCGCATCTAGATACAAAGTTGTCTAACTGGGCATATCAAC 660

```

```

DB 601 GTCTGCTTACCAATGAGCGCATCTAGATACAAAGTTGTCTAACTGGGCATATCAAC 660
QY 661 AGGTCCAAAGAAATTAAGAAAGATGCTGCTGATTAAGATATTTTGAAGATGAATTT 720
DB 661 AGGTCCAAAGAAATTAAGAAAGATGCTGCTGATTAAGATATTTTGAAGATGAATTT 720
QY 721 ATGTGCTCTGGGAATTTGGGATTTGGCAATGCTGCTGTTGGCTGACATCTATTC 780
DB 721 ATGTGCTCTGGGAATTTGGGATTTGGCAATGCTGCTGTTGGCTGACATCTATTC 780
QY 781 CATCTGAGTGAATCTTTGACATGAGAGAAATTTCACTATATTCAGACCAAGCTAGAA 840
DB 781 CATCTGAGTGAATCTTTGACATGAGAGAAATTTCACTATATTCAGACCAAGCTAGAA 840
QY 841 TTGTTTCCCTTCTGCTGAGGCAATACAGCATTTATTTTGGCTGGAAATAGTGATG 900
DB 841 TTGTTTCCCTTCTGCTGAGGCAATACAGCATTTATTTTGGCTGGAAATAGTGATG 900
QY 901 ATATAAACAATTTGATGATATACACCTCCAACTTTATGATGATGCTTTTCTCCAA 960
DB 901 ATATAAACAATTTGATGATATACACCTCCAACTTTATGATGATGCTTTTCTCCAA 960
QY 961 TTGTTTCCCTGATATTTAAAGCATATCTATTCCTGCACTTTGAGAAAGATACGTA 1020
DB 961 TTGTTTCCCTGATATTTAAAGCATATCTATTCCTGCACTTTGAGAAAGATACGTA 1020
QY 1021 AGATTAGACATGTTGGGAAAGCTGACCAAAATTAACAAACTGATATGTTCCAGT 1080
DB 1021 AGATTAGACATGTTGGGAAAGCTGACCAAAATTAACAAACTGATATGTTCCAGT 1080
QY 1081 TGTAGAAATTAATGTTTACACATTTTGTCAATATGATATTTATATTTATACCAACAT 1140
DB 1081 TGTAGAAATTAATGTTTACACATTTTGTCAATATGATATTTATATTTATACCAACAT 1140
QY 1141 TCAAGTTTGTATTTGTTAAATTAATGATTAATTCAGAGAAAAAATTTTAAAAA 1195
DB 1141 TCAAGTTTGTATTTGTTAAATTAATGATTAATTCAGAGAAAAAATTTTAAAAA 1195

```

```

RESULT 6
US-10-012-896-878
; Sequence 878, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yudi
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Mantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896

```

CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-878

Query Match 100.0%; Score 1195; DB 5; Length 1195;

Best Local Similarity 100.0%; Pred. No. 1,1e-281; Mismatches 0; Indels 0; Gaps 0;

Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCGAGACTCAGCGTCAAGCTTAGGGGAGAGAGTGGGTGGTGAAGCCATCTATTTATAG 60
DB 1 CCGAGACTCAGCGTCAAGCTTAGGGGAGAGAGTGGGTGGTGAAGCCATCTATTTATAG 60
QY 61 AATTATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 61 AATTATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 121 GGAGAAATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 GGAGAAATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 AAAGACCTGCTTGTGATTTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 AAAGACCTGCTTGTGATTTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 CAGAACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 CAGAACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 CTATTATAGCATCTCTGACCTTTCTTACACTCTTCTGAGGAGAGAGAGAGAGAGAG 360
DB 301 CTATTATAGCATCTCTGACCTTTCTTACACTCTTCTGAGGAGAGAGAGAGAGAGAG 360
QY 361 CAACCTCCATCAACAAATTTTAAATTCGAATCTGATCAACAAAGCTTTC 420
DB 361 CAACCTCCATCAACAAATTTTAAATTCGAATCTGATCAACAAAGCTTTC 420
QY 421 CAATGGTTTCATCACTCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 CAATGGTTTCATCACTCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 TCCAACTTCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 TCCAACTTCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 TAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 TAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 GTCTGTCTTACCAATGAGGCGATCTTACAGATTAAGAGAGAGAGAGAGAGAGAG 660
DB 601 GTCTGTCTTACCAATGAGGCGATCTTACAGATTAAGAGAGAGAGAGAGAGAGAG 660
QY 661 AGGTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 AGGTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 ATGTGTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 ATGTGTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 CATCTGTGAGTGAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 CATCTGTGAGTGAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 TTGTTTCCCTTCTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 TTGTTTCCCTTCTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
```

```
QY 901 ATATMAAACATTTGTATGTATACACCTCCACTTTTATGATAGCTGTTTCTTCCAA 960
DB 901 ATATMAAACATTTGTATGTATACACCTCCACTTTTATGATAGCTGTTTCTTCCAA 960
QY 961 TTGTTTCCCTTCTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 TTGTTTCCCTTCTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 AGATTAGCATGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 AGATTAGCATGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 TGTAGAAATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1081 TGTAGAAATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
```

RESULT 7

US-10-011-095-1
Sequence 1, Application US/10011095
Publication No. US20030045682A1
GENERAL INFORMATION:
APPLICANT: Hubert, Daniel
APPLICANT: Afar, Rene S.
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arthur B.
APPLICANT: Saittan, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAP1 (AS AMENDED)
FILE REFERENCE: 511582001610
CURRENT APPLICATION NUMBER: US/10/011,095
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-011-095-1

Query Match 100.0%; Score 1195; DB 5; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1,1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CCGAGACTCAGCGTCAAGCTTAGGGGAGAGAGTGGGTGGTGAAGCCATCTATTTATAG 60
DB 1 CCGAGACTCAGCGTCAAGCTTAGGGGAGAGAGTGGGTGGTGAAGCCATCTATTTATAG 60
QY 61 AATTATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 61 AATTATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 121 GGAGAAATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 GGAGAAATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 AAAGACCTGCTTGTGATTTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 AAAGACCTGCTTGTGATTTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 CAGAACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 CAGAACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
```

```

QY 301 CTATATAGCATCTGACTTTTCTTACACTCTTCTGAGGAGTAATTCACCCCTTAG 360
    |||
Db 301 CTATATAGCATCTGACTTTTCTTACACTCTTCTGAGGAGTAATTCACCCCTTAG 360
QY 361 CAACCTCCCATCAACAATATTTTATTAATAATTCACATCTGTCATCAACAAAGTCTGC 420
    |||
Db 361 CAACCTCCCATCAACAATATTTTATTAATAATTCACATCTGTCATCAACAAAGTCTGC 420
QY 421 CAATGTTTCCATCACTCTCTTGGCAATGGTTTACCTGCGCAGAGTGATAGCAATTC 480
    |||
Db 421 CAATGTTTCCATCACTCTCTTGGCAATGGTTTACCTGCGCAGAGTGATAGCAATTC 480
QY 481 TCCAACTTCATATGGAACCAAGATATTAAGAAAGTTTCCAACTGGTTGATAGTGATG 540
    |||
Db 481 TCCAACTTCATATGGAACCAAGATATTAAGAAAGTTTCCAACTGGTTGATAGTGATG 540
QY 541 TAAACAAGAAAGAGTTGGGCTTCTCAGTTCTTTTCTGCTGACTGATGCAATTTATA 600
    |||
Db 541 TAAACAAGAAAGAGTTGGGCTTCTCAGTTCTTTTCTGCTGACTGATGCAATTTATA 600
QY 601 GTCTGTCTTAACCAATGAGGCGATCTTACAGATACAAAGTTGCTMAACTGGGCAATAC 660
    |||
Db 601 GTCTGTCTTAACCAATGAGGCGATCTTACAGATACAAAGTTGCTMAACTGGGCAATAC 660
QY 661 AGGTCCAAACAAATTAAGAAAGATGCGCTGATGAGCATGATGTTGGAGAAATGAGATT 720
    |||
Db 661 AGGTCCAAACAAATTAAGAAAGATGCGCTGATGAGCATGATGTTGGAGAAATGAGATT 720
QY 721 ATGTGCTCTGGAATTTGTGGAAATTTGGCAATAGCTGCTGTTGGCTGATCTTAATTC 780
    |||
Db 721 ATGTGCTCTGGAATTTGTGGAAATTTGGCAATAGCTGCTGTTGGCTGATCTTAATTC 780
QY 781 CATCTGTGAGTGACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCACTAGGAA 840
    |||
Db 781 CATCTGTGAGTGACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCACTAGGAA 840
QY 841 TTGTTTCCCTTCTACTGAGGACAAATACAGCAATTTGCTGCGAATTAAGTGATG 900
    |||
Db 841 TTGTTTCCCTTCTACTGAGGACAAATACAGCAATTTGCTGCGAATTAAGTGATG 900
QY 901 ATATATAACAAATTTGTATGATATACACTTCCAACTTTTATGATAGCTGTTTCTTCCA 960
    |||
Db 901 ATATATAACAAATTTGTATGATATACACTTCCAACTTTTATGATAGCTGTTTCTTCCA 960
QY 961 TTGTTTCTGATATTTTAAAGCATACTATCTCTGCCATGCTTGAAGAGAAATCTGA 1020
    |||
Db 961 TTGTTTCTGATATTTTAAAGCATACTATCTCTGCCATGCTTGAAGAGAAATCTGA 1020
QY 1021 AGATTAGACATGGTTGGGAAGAGCTACCAAAATTAACAAACCTGAGATATGTTCCAGT 1080
    |||
Db 1021 AGATTAGACATGGTTGGGAAGAGCTACCAAAATTAACAAACCTGAGATATGTTCCAGT 1080
QY 1081 TGTAGAAATTAAGTTTACACAACTTTTGTTCATAATATGATATTTTATCACCAATTC 1140
    |||
Db 1081 TGTAGAAATTAAGTTTACACAACTTTTGTTCATAATATGATATTTTATCACCAATTC 1140
QY 1141 TCAAGTTTGTATTTGTTAATAAATGATTTTCAAGAAAAAATTTTAAAAA 1195
    |||
Db 1141 TCAAGTTTGTATTTGTTAATAAATGATTTTCAAGAAAAAATTTTAAAAA 1195

```

RESULT 8

```

US-10-010-667A-1
; Sequence 1, Application US/10010667A
; Publication No. US20030055217A1
; GENERAL INFORMATION:
; APPLICANT: Afeir, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saifran, Douglas C.
; APPLICANT: Mitchell, Steve Chapell

```

```

; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; FILE REFERENCE: 511582001601
; CURRENT APPLICATION NUMBER: US/10/010,667A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-010-667A-1

Query Match      100.0%; Score 1195; DB 5; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1,1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGAGACTCAGCGCTAAGCTAAGCGGAGAGTGGTGCTGAAGCCATATTTATAG 60
    |||
Db 1 CCGAGACTCAGCGCTAAGCTAAGCGGAGAGTGGTGCTGAAGCCATATTTATAG 60
QY 61 AATTATGGAAGCAGAAAAAGCATCAACAACCAAGAAATCTTTGAAATTAAGCCTTA 120
    |||
Db 61 AATTATGGAAGCAGAAAAAGCATCAACAACCAAGAAATCTTTGAAATTAAGCCTTA 120
QY 121 GGAGAAATTTAGAAAGAGCATTTATTTGATTAAGGACAGGAGAGACAGCATCTTA 180
    |||
Db 121 GGAGAAATTTAGAAAGAGCATTTATTTGATTAAGGACAGGAGAGACAGCATCTTA 180
QY 181 AAAGACTGTGCTTTTGATTTGCAACCAACAGCCCATCTGATGATTTGACTGCTT 240
    |||
Db 181 AAAGACTGTGCTTTTGATTTGCAACCAACAGCCCATCTGATGATTTGACTGCTT 240
QY 241 CAGAACTTACGACACACAGAACTTTTCCACAGTGGCACTTCCAAATTAATATGCTG 300
    |||
Db 241 CAGAACTTACGACACACAGAACTTTTCCACAGTGGCACTTCCAAATTAATATGCTG 300
QY 301 CTATATAGCATCTGACTTTTCTTACACTCTTCTGAGGAGTAATTCACCCCTTAG 360
    |||
Db 301 CTATATAGCATCTGACTTTTCTTACACTCTTCTGAGGAGTAATTCACCCCTTAG 360
QY 361 CAACCTCCCATCAACAATATTTTATTAATAATTCACATCTGTCATCAACAAAGTCTGC 420
    |||
Db 361 CAACCTCCCATCAACAATATTTTATTAATAATTCACATCTGTCATCAACAAAGTCTGC 420
QY 421 CAATGTTTCCATCACTCTCTTGGCAATGGTTTACCTGCGCAGAGTGATAGCAATTC 480
    |||
Db 421 CAATGTTTCCATCACTCTCTTGGCAATGGTTTACCTGCGCAGAGTGATAGCAATTC 480
QY 481 TCCAACTTCATATGGAACCAAGATATTAAGAAAGTTTCCAACTGGTTGATAGTGATG 540
    |||
Db 481 TCCAACTTCATATGGAACCAAGATATTAAGAAAGTTTCCAACTGGTTGATAGTGATG 540
QY 541 TAAACAAGAAAGAGTTGGGCTTCTCAGTTCTTTTCTGCTGACTGATGCAATTTATA 600
    |||
Db 541 TAAACAAGAAAGAGTTGGGCTTCTCAGTTCTTTTCTGCTGACTGATGCAATTTATA 600
QY 601 GTCTGTCTTAACCAATGAGGCGATCTTACAGATACAAAGTTGCTMAACTGGGCAATAC 660
    |||
Db 601 GTCTGTCTTAACCAATGAGGCGATCTTACAGATACAAAGTTGCTMAACTGGGCAATAC 660
QY 661 AGGTCCAAACAAATTAAGAAAGATGCGCTGATGAGCATGATGTTGGAGAAATGAGATT 720
    |||
Db 661 AGGTCCAAACAAATTAAGAAAGATGCGCTGATGAGCATGATGTTGGAGAAATGAGATT 720
QY 721 ATGTGCTCTGGAATTTGTGGAAATTTGGCAATAGCTGCTGTTGGCTGATCTTAATTC 780
    |||

```

Db 721 ATGTCTCTGGAAATTGGGAATTGGCAATACCTGGCTCTGTGGCTGTGACATCTATTTC 780
Qy 781 CATCTGTGAGTACTCTTTGACATGAGAGAAATTTCACTATATTGACAGCAAGTAGGAA 840
Db 781 CATCTGTGAGTACTCTTTGACATGAGAGAAATTTCACTATATTGACAGCAAGTAGGAA 840
Qy 841 TTGTTTCCCTTCTACTGGGCAATACAGCATTTGTTTGCCTGGAAATAGTGATAG 900
Db 841 TTGTTTCCCTTCTACTGGGCAATACAGCATTTGTTTGCCTGGAAATAGTGATAG 900
Qy 901 AATATAAACAAATTTGATAGTATATACACCTCCAACTTTATGATAGTGTTCCTCCAA 960
Db 901 AATATAAACAAATTTGATAGTATATACACCTCCAACTTTATGATAGTGTTCCTCCAA 960
Qy 961 TTGTTTCCCTGATATTTAAAGCATATCTATTCCTGGCATGCTTGAGGAAGAAATACGA 1020
Db 961 TTGTTTCCCTGATATTTAAAGCATATCTATTCCTGGCATGCTTGAGGAAGAAATACGA 1020
Qy 1021 AGATTAGACATGTTGGGAAGACGTACCAAAATTAACAAAACGTAGATATGTTCCAGT 1080
Db 1021 AGATTAGACATGTTGGGAAGACGTACCAAAATTAACAAAACGTAGATATGTTCCAGT 1080
Qy 1081 TGTAGAAATTAAGTATTAACACATTTTGTCAATATGATATATTTATACCAACATTT 1140
Db 1081 TGTAGAAATTAAGTATTAACACATTTTGTCAATATGATATATTTATACCAACATTT 1140
Qy 1141 TCAAGTTTGTATTTGTTAATTAATGATTTCAAGAAAAAATTTTAAAAA 1195
Db 1141 TCAAGTTTGTATTTGTTAATTAATGATTTCAAGAAAAAATTTTAAAAA 1195

RESULT 9
US-10-205-823-396

Sequence 396, Application US/10205823
Publication No. US20030108963A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbacheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangit
APPLICANT: Moneey, Angela M.
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FaestSeq for Windows Version 4.0
SEQ ID NO 396
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-10-205-823-396

Query Match 100.0%; Score 1195; DB 5; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1,1e-281;

Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGAGACTCAGGTCACGCTAAAGCGAAGAGTGGTGGCTGAAGCCATATTTTATAG 60
Db 1 CCGAGACTCAGGTCACGCTAAAGCGAAGAGTGGTGGCTGAAGCCATATTTTATAG 60
Qy 61 AATTATGGAAGCAAGAAAGCATCAACCAAGAAAGAACTTTGAAAAATGAAGCCCA 120
Db 61 AATTATGGAAGCAAGAAAGCATCAACCAAGAAAGAACTTTGAAAAATGAAGCCCA 120
Qy 121 GGAGAAATTTAGAAAGACGATTTATTTGATTAAGAGACGGGAGAGACGACATGTCTAA 180
Db 121 GGAGAAATTTAGAAAGACGATTTATTTGATTAAGAGACGGGAGAGACGACATGTCTAA 180
Qy 181 AAAAGACTGTGCTTTTGCAATTTGACCAAAAGCCCATGCTGATGAATTTGACGCTCT 240
Db 181 AAAAGACTGTGCTTTTGCAATTTGACCAAAAGCCCATGCTGATGAATTTGACGCTCT 240
Qy 241 CAGAACTTCAGACACACAGAAAGCTTTCCACAGTGGCACTTGCATTTAAATAGCG 300
Db 241 CAGAACTTCAGACACACAGAAAGCTTTCCACAGTGGCACTTGCATTTAAATAGCG 300
Qy 301 CTATTATAGCATCTCTGACTTTCTTTACACTCTCTGAGGGAATTAATTCACCTTTAG 360
Db 301 CTATTATAGCATCTCTGACTTTCTTTACACTCTCTGAGGGAATTAATTCACCTTTAG 360
Qy 361 CAACCTCCCATCAACATATTTTAAATTCGAATCTGTGATCAACAAAGCTTGC 420
Db 361 CAACCTCCCATCAACATATTTTAAATTCGAATCTGTGATCAACAAAGCTTGC 420
Qy 421 CAATGTTTCCATCTCTCTTTGGCATGTTTACCTGCGAGTGTGATAGAGCAATTG 480
Db 421 CAATGTTTCCATCTCTCTTTGGCATGTTTACCTGCGAGTGTGATAGAGCAATTG 480
Qy 481 TCCAACTTCATATGGAACCAAGTATTAAGAGTTTCCACATTTGTTGATTAAGTGAAT 540
Db 481 TCCAACTTCATATGGAACCAAGTATTAAGAGTTTCCACATTTGTTGATTAAGTGAAT 540
Qy 541 TAAACAAGAAAGCAGTTTGGCTTCTCAAGTTCTTTTGTCTGTACTGATGCAATTTATA 600
Db 541 TAAACAAGAAAGCAGTTTGGCTTCTCAAGTTCTTTTGTCTGTACTGATGCAATTTATA 600
Qy 601 GTCTGTCTTACCCATAGAGGCGATCTCAAGTAAAGTGTCTAACTGGGCAATATCAAC 660
Db 601 GTCTGTCTTACCCATAGAGGCGATCTCAAGTAAAGTGTCTAACTGGGCAATATCAAC 660
Qy 661 AGSTCAACAAATTAAGAAAGATGCTGGATTAAGCATGATGTTTGAATGAGATTT 720
Db 661 AGSTCAACAAATTAAGAAAGATGCTGGATTAAGCATGATGTTTGAATGAGATTT 720
Qy 721 ATGTCTCTGGAAATGTGGATTGGCAATACGCTCTGTGTGGCTGTGACATCTATTC 780
Db 721 ATGTCTCTGGAAATGTGGATTGGCAATACGCTCTGTGTGGCTGTGACATCTATTC 780
Qy 781 CATCTGTGAGTACTCTTTGACATGAGAGAAATTTCACTATTTGACAGCAAGTAGGAA 840
Db 781 CATCTGTGAGTACTCTTTGACATGAGAGAAATTTCACTATTTGACAGCAAGTAGGAA 840
Qy 841 TTGTTTCCCTTCTACTGGGCAATACAGCATTTGTTTGCCTGGAAATAGTGATAG 900
Db 841 TTGTTTCCCTTCTACTGGGCAATACAGCATTTGTTTGCCTGGAAATAGTGATAG 900
Qy 901 AATATAAACAAATTTGATAGTATATACACCTCCAACTTTATGATAGTGTTCCTCCAA 960
Db 901 AATATAAACAAATTTGATAGTATATACACCTCCAACTTTATGATAGTGTTCCTCCAA 960
Qy 961 TTGTTTCCCTGATATTTAAAGCATATCTATTCCTGGCATGCTTGAGGAAGAAATACGA 1020
Db 961 TTGTTTCCCTGATATTTAAAGCATATCTATTCCTGGCATGCTTGAGGAAGAAATACGA 1020
Qy 1021 AGATTAGACATGTTGGGAAGACGTACCAAAATTAACAAAACGTAGATATGTTCCAGT 1080
Db 1021 AGATTAGACATGTTGGGAAGACGTACCAAAATTAACAAAACGTAGATATGTTCCAGT 1080

Oy	1081	TGAGAAATTACGTGTTCACCAATTTTGGTCAATATGATATATTATATCCAACTT	1144
Dd	1081	TGTGAATTAATCAGTTTACACACTTTTGTTCAATATGATATATTATATCCAACTT	1140
Oy	1141	TCAAGTTTGTATTTGTTAATAATAATGATTAATTCAGAAGAAAAA	1195
Dd	1141	TCAAGTTTGTATTTGTTAATAATAATGATTAATTCAGAAGAAAAA	1195
 RESULT 10 US-10-144-678A-878 ; Sequence 878, Application US/10144678A ; Publication No. US20030157089A1 ; GENERAL INFORMATION: ; APPLICANT: Xu, Jiangchun ; APPLICANT: Dillon, Devin C. ; APPLICANT: Mitcham, Jennifer L. ; APPLICANT: Harlocker, Susan L. ; APPLICANT: Jiang, Yugu ; APPLICANT: Henderson, Robert A. ; APPLICANT: Kalos, Michael D. ; APPLICANT: Fanger, Gary R. ; APPLICANT: Retter, Marc W. ; APPLICANT: Stolk, John A. ; APPLICANT: Day, Craig H. ; APPLICANT: Vedvick, Thomas S. ; APPLICANT: Carter, Darlick ; APPLICANT: Li, Samuel X. ; APPLICANT: Wang, Aljun ; APPLICANT: Skeiky, Yasir A. W. ; APPLICANT: Hepler, William T. ; APPLICANT: Hurral, John ; APPLICANT: McNeill, Patricia D. ; APPLICANT: Houghton, Raymond L. ; APPLICANT: Vinales y de Bassols, Carlota ; APPLICANT: Foy, Teresa M. ; APPLICANT: Watanabe, Yoshihiro ; APPLICANT: Deng, Ta ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND ; FILE REFERENCE: 210121.427C28 ; CURRENT APPLICATION NUMBER: US/10/144, 678A ; CURRENT FILING DATE: 2002-08-12 ; NUMBER OF SEQ ID NOS: 1033 ; SOFTWARE: FastSeq for Windows Version 3.0 ; SEQ ID NO 878 ; LENGTH: 1195 ; TYPE: DNA ; ORGANISM: Homo sapiens ; US-10-144-678A-878			
Oy	Query Match	100.0%; Score 1195; DB 6; Length 1195;	
Oy	Best Local Similarity	100.0%; Pred. No. 1.le-281;	
Dd	Matches 1195;	Consecutive 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1	CCGAGACTCACCGGTCAAGCTTAAGCGGAAGTGGGTGGCTGAAGCCATCTATTATTTTAG	60
Dd	1	CCGAGACTCACGGTCAAGCTTAAGCGGAAGTGGGTGGCTGAAGCCATCTATTATTTTAG	60
Oy	61	AATTATGGAAGACGAAAAGACATCAAAACCAGAAGAACTTTGGAAAATGAAGCTTA	120
Dd	61	AATTATGGAAGACGAAAAGACATCAAAACCAGAAGAACTTTGGAAAATGAAGCTTA	120
Oy	121	GGAAGAAATTTTGAAGAAAGACATTTATTTTGCATAAGACAAGGGAAGAACCGCATGCTAA	180
Dd	121	GGAAGAAATTTTGAAGAAAGACATTTATTTTGCATAAGACAAGGGAAGAACCGCATGCTAA	180
Oy	181	AAAGACCTGTGCTTTTGCATTTGCACCAAACAGGCCATGCTGATGAATTTTGAATGACCTT	240
Dd	181	AAAGACCTGTGCTTTTGCATTTTGCACCAAACAGGCCATGCTGATGAATTTTGAATGACCTT	240
Oy	241	CAGAACTTCAGACACACAGAACTCTTTCCACAGTGGCACTTCCCAATTAATTAAGCTG	300

D	b		241	CAGAACTTCAGCACAACAGGAATCTTTCCACGTCGGCACTTGCATTTAAATTAGCTG	300
O	y		301	CTATTTAAGCATCTCGACTTTTCTTTTACACTCTTGTGAGGGAAGTAATTCACCCTTTAG	360
D	b		301	CTATTTAAGCATCTCTGACTTTTCTTTAACCTCTTGAGGGGAAGTAATTCACCCTTTAG	360
O	y		361	CAACTTCCCACCAACAAATTTTTATAAATTCGAATCCGTGTCATCAACAAATCTTGC	420
D	b		361	CAACTTCCCACCAACAAATTTTTATAAATTCGAATCCGTGTCATCAACAAATCTTGC	420
O	y		421	CAATGTTTTCATCACTCTCTTGGCATTTGGTTTACCTGCCAGGCGTATAGCAGCAATTG	480
D	b		421	CAATGTTTTCATCACTCTCTTGGCATTTGGTTTACCTGCCAGGCGTATAGCAGCAATTG	480
O	y		481	TCCAATCTCATATATGGAACCAAGTATAGAAGTTTCACATTTGGTTGATTAAGTAGT	540
D	b		481	TCCAATCTCATATATGGAACCAAGTATAGAAGTTTCACATTTGGTTGATTAAGTAGT	540
O	y		541	TAAACAAGAAAGCAATTTGGGCTTCTCAGTTTCTTTTGTCTGTACTGCAATGCAATTTATA	600
D	b		541	TAAACAAGAAAGCAATTTGGGCTTCTCAGTTTCTTTTGTCTGTACTGCAATGCAATTTATA	600
O	y		601	GTCGTGCTTACCCCAATGAGGCGATCCCAACAGATACAAGTTGCTTAACTGGGCAATACAC	660
D	b		601	GTCGTGCTTACCCCAATGAGGCGATCCCAACAGATACAAGTTGCTTAACTGGGCAATACAC	660
O	y		661	AGGTCCAACAAAATPAAAGAAAGATGCCCTGATTTGACATGATGTTTGGAGAATGGAGATT	720
D	b		661	AGGTCCAACAAAATPAAAGAAAGATGCCCTGATTTGACATGATGTTTGGAGAATGGAGATT	720
O	y		721	ATGTGCTCTCGGGAATTTGTGGATTTGGCAATACCTGGCTCTGTTGGCTGTACATCTATTC	780
D	b		721	ATGTGCTCTCGGGAATTTGTGGATTTGGCAATACCTGGCTCTGTTGGCTGTACATCTATTC	780
O	y		781	CATCTGAGAGTACTCTTTGACATGAGAGAAATTTCACTATTTACAGAGCAAGCTTAGAA	840
D	b		781	CATCTGAGAGTACTCTTTGACATGAGAGAAATTTCACTATTTACAGAGCAAGCTTAGAA	840
O	y		841	TTGTGTTCCCTTCTTACTGGGCAACAATACGCAATTTGATTTTGGCTGGAAATAGTGATAG	900
D	b		841	TTGTGTTCCCTTCTTACTGGGCAACAATACGCAATTTGATTTTGGCTGGAAATAGTGATAG	900
O	y		901	ATATPAAAACAATTTGTATGSGTATACACCTCCAACTTTATGATAGCTGTTTCTCTCAA	960
D	b		901	ATATPAAAACAATTTGTATGSGTATACACCTCCAACTTTATGATAGCTGTTTCTCTCAA	960
O	y		961	TTGTGTTCCCTGATTTTAAAGCATTAATTCCTGCGCATCTTGAGGAAAGATVACTGA	1020
D	b		961	TTGTGTTCCCTGATTTTAAAGCATTAATTCCTGCGCATCTTGAGGAAAGATVACTGA	1020
O	y		1021	AGATTTAGACATGTTGGGGAAGACGTCAACCAAAATTAACAACCTGAGATATGTTCCAGT	1080
D	b		1021	AGATTTAGACATGTTGGGGAAGACGTCAACCAAAATTAACAACCTGAGATATGTTCCAGT	1080
O	y		1081	TGTAGAAATTAATGTTTACACAAATTTTGTTCATATATGATATATTTTATCACCAATTT	1140
D	b		1081	TGTAGAAATTAATGTTTACACAAATTTTGTTCATATATGATATATTTTATCACCAATTT	1140
O	y		1141	TCAAGTTTGTATTTGTTTAAATTAATGATTTTACAGGAAAAAAAAAAAAAAAAAAAA	1195
D	b		1141	TCAAGTTTGTATTTGTTTAAATTAATGATTTTACAGGAAAAAAAAAAAAAAAAAAAA	1195
RESULT 11					
US-10-294-025-878					
; Sequence 878, Application US/10294025					
; Publication No. US20030185830A1					
; GENERAL INFORMATION:					
; APPLICANT: Xu, Jiangchun					
; APPLICANT: Stolc, John A.					
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND					

;; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;; FILE REFERENCE: 210121.427C29
;; CURRENT APPLICATION NUMBER: US/10/294,025
;; CURRENT FILING DATE: 2002-11-12
;; NUMBER OF SEQ ID NOS: 1038
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 878
;; LENGTH: 1195
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-294-025-878

Query Match 100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1.1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCGAGACTCAGCGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATCTATTTATAG 60
DB 1 CCGAGACTCAGCGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATCTATTTATAG 60
QY 61 AATTATGGAAGCAGAAAAAGCATCAAAACCAAGAAAGACTTTGGAAAATGAAGCTTA 120
DB 61 AATTATGGAAGCAGAAAAAGCATCAAAACCAAGAAAGACTTTGGAAAATGAAGCTTA 120
QY 121 GGAGAAATTTAGAGAGAGCATTTATTTGCATTAAGGACCGGAGAGACCAAGCTTA 180
DB 121 GGAGAAATTTAGAGAGAGCATTTATTTGCATTAAGGACCGGAGAGACCAAGCTTA 180
QY 181 AAAAGCTGTGCTTTTGCATTTTGCACCAAAAGCCCATCTGTGAATTTGACGCTT 240
DB 181 AAAAGCTGTGCTTTTGCATTTTGCACCAAAAGCCCATCTGTGAATTTGACGCTT 240
QY 241 CAGAACTTCAGACACACAGAACTTTTCCAAGTGGGACTTCCCAATTAATAATAGCTG 300
DB 241 CAGAACTTCAGACACACAGAACTTTTCCAAGTGGGACTTCCCAATTAATAATAGCTG 300
QY 301 CTAATTATAGCATCTCTGACTTTTCTTTTACACTCTTTCTGAGGGAAGTAATTCACCCCTT 360
DB 301 CTAATTATAGCATCTCTGACTTTTCTTTTACACTCTTTCTGAGGGAAGTAATTCACCCCTT 360
QY 361 CAACCTCCCATCAACAAATATTTTATTAATAATTCCTGGGATCAACAAGTCTTGC 420
DB 361 CAACCTCCCATCAACAAATATTTTATTAATAATTCCTGGGATCAACAAGTCTTGC 420
QY 421 CAATGTTTCCATCACTCTCTTGGCATTTGGTTTACCTGCGAGGTGTGATAGCAGCAATTG 480
DB 421 CAATGTTTCCATCACTCTCTTGGCATTTGGTTTACCTGCGAGGTGTGATAGCAGCAATTG 480
QY 481 TCCAACTTATATGGAACCAAGTATTAAGAAGTTTCCAACTTGGTGGATAGTGAATGT 540
DB 481 TCCAACTTATATGGAACCAAGTATTAAGAAGTTTCCAACTTGGTGGATAGTGAATGT 540
QY 541 TAAACAAGAAAGAGTTGGGCTTCTCAGTTTCTTTTGTCTGTACTGATGCAATTTATA 600
DB 541 TAAACAAGAAAGAGTTGGGCTTCTCAGTTTCTTTTGTCTGTACTGATGCAATTTATA 600
QY 601 GTCTGTCTTACCAATGAGCGCATCTCAAGATACAAAGTTGCTAAACTGGGCATATCAAC 660
DB 601 GTCTGTCTTACCAATGAGCGCATCTCAAGATACAAAGTTGCTAAACTGGGCATATCAAC 660
QY 661 AGGTCCAAAGAAATTAAGAAGATGCTGATTTGAAGATATGTTTGAAGATGGAATTT 720
DB 661 AGGTCCAAAGAAATTAAGAAGATGCTGATTTGAAGATATGTTTGAAGATGGAATTT 720
QY 721 ATGTGCTCTGGGAATTTGGGATTTGGCAATACTGGCTGTGTGGCTGTGACATCTAATTC 780
DB 721 ATGTGCTCTGGGAATTTGGGATTTGGCAATACTGGCTGTGTGGCTGTGACATCTAATTC 780
QY 781 CATCTGTGAGTGACTCTTTTGAATGAGAAATTTCACTATATTCAGAGCAAGCTAGAA 840
DB 781 CATCTGTGAGTGACTCTTTTGAATGAGAAATTTCACTATATTCAGAGCAAGCTAGAA 840
QY 841 TTGTTTCCCTTCTACTGGGCAATACAGCATTTGATTTTGTGCTGGAATTAAGTGAATAG 900
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DB 841 TTGTTTCCCTTCTACTGGGCAATACAGCATTTGATTTTGTGCTGGAAATAGTGAATAG 900
QY 901 ATATAAAAAATTTGTATGTATACACCTCCAACTTTTATGATAGTGTTCCTCCAA 960
DB 901 ATATAAAAAATTTGTATGTATACACCTCCAACTTTTATGATAGTGTTCCTCCAA 960
QY 961 TTGTTGCTCTGATATTTAAAAAGCATCTATTTCTGCGCATGCTTGAGAAAGATATCGA 1020
DB 961 TTGTTGCTCTGATATTTAAAAAGCATCTATTTCTGCGCATGCTTGAGAAAGATATCGA 1020
QY 1021 AGATTAGCATGTTGGGAGAGCGTCAACCAAAATTAACAAACTGAGATATGTTCCAGT 1080
DB 1021 AGATTAGCATGTTGGGAGAGCGTCAACCAAAATTAACAAACTGAGATATGTTCCAGT 1080
QY 1081 TGTAGAAATTAATCTGTTTACACACATTTTGTTCATATATGATATTTATATGACCAACAT 1140
DB 1081 TGTAGAAATTAATCTGTTTACACACATTTTGTTCATATATGATATTTATATGACCAACAT 1140
QY 1141 TCAAGTTGTATTTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1195
DB 1141 TCAAGTTGTATTTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1195
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RESULT 12
US-10-393-590-35
; Sequence 35, Application US/10393590
; Publication No. US20030190656a1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNASTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,789
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: human
US-10-393-590-35

Query Match 100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1.1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCGAGACTCAGCGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATCTATTTATAG 60
DB 1 CCGAGACTCAGCGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATCTATTTATAG 60
QY 61 AATTATGGAAGCAGAAAAAGCATCAAAACCAAGAAAGACTTTGAAAATGAAGCTTA 120
DB 61 AATTATGGAAGCAGAAAAAGCATCAAAACCAAGAAAGACTTTGAAAATGAAGCTTA 120
QY 121 GGAGAAATTTAGAGAGAGCATTTATTTGCATTAAGGACCGGAGAGACCAAGCTTA 180
DB 121 GGAGAAATTTAGAGAGAGCATTTATTTGCATTAAGGACCGGAGAGACCAAGCTTA 180
QY 181 AAAAGCTGTGCTTTTGCATTTTGCACCAAAAGCCCATCTGTGAATTTGACGCTT 240
DB 181 AAAAGCTGTGCTTTTGCATTTTGCACCAAAAGCCCATCTGTGAATTTGACGCTT 240
QY 241 CAGAACTTCAGACACACAGAACTTTTCCAAGTGGGACTTCCCAATTAATAATAGCTG 300
DB 241 CAGAACTTCAGACACACAGAACTTTTCCAAGTGGGACTTCCCAATTAATAATAGCTG 300
QY 301 CTAATTATAGCATCTCTGACTTTTCTTTTACACTCTTTCTGAGGGAAGTAATTCACCCCTT 360
DB 301 CTAATTATAGCATCTCTGACTTTTCTTTTACACTCTTTCTGAGGGAAGTAATTCACCCCTT 360
QY 361 CAACCTCCCATCAACAAATATTTTATTAATAATTCATCTGTGATCAACAAGTCTTGC 420
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ORGANISM: human		US-10-393-567-35	
Query Match	100.0%; Score 1195; DB 6; Length 1195;		
Best Local Similarity	100.0%; Pred. No. 1,1e-281;		
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
QY	1	CCGAGACTCAGGCTCAAGCTTAAGCGGAAGAGTGGGTGGCTGAAGCCATACATATTTTATAG	60
DB	1	CCGAGACTCAGGCTCAAGCTTAAGCGGAAGAGTGGGTGGCTGAAGCCATACATATTTTATAG	60
QY	61	AATTAAATGGAAGCAGAAAAGACATCAACAAACCAAGAGAACTTTGGAAAAATGAAGCCTTA	120
DB	61	AATTAAATGGAAGCAGAAAAGACATCAACAAACCAAGAGAACTTTGGAAAAATGAAGCCTTA	120
QY	121	GGAGAAATTTTGAAGAAAGACATATTTTGGCTAAAGACACGGGAGAGACCAGCATGCTTAA	180
DB	121	GGAGAAATTTTGAAGAAAGACATATTTTGGCTAAAGACACGGGAGAGACCAGCATGCTTAA	180
QY	181	AAAGACCTGTGCTTTTGGCATTTGGACCCAAACAGCCATGCTGAATGAAATTTTACATGCTT	240
DB	181	AAAGACCTGTGCTTTTGGCATTTGGACCCAAACAGCCATGCTGAATGAAATTTTACATGCTT	240
QY	241	CAGAACTTCAGCACACAGGAACCTCTTCCACAGTGGCATTGCCAATTAATAATAGCTG	300
DB	241	CAGAACTTCAGCACACAGGAACCTCTTCCACAGTGGCATTGCCAATTAATAATAGCTG	300
QY	301	CTATTATAGCATCTCTGACTTTTCTTTAACACTCTTGAGGGAAGTAAATTCACCCTTTAG	360
DB	301	CTATTATAGCATCTCTGACTTTTCTTTAACACTCTTGAGGGAAGTAAATTCACCCTTTAG	360
QY	361	CAACTTCCCATCAACAAATATTTTATTAATAATTCMAATCTTGATCATCAACAAAGCTTTC	420
DB	361	CAACTTCCCATCAACAAATATTTTATTAATAATTCMAATCTTGATCATCAACAAAGCTTTC	420
QY	421	CAATGTTTCCATCACTCTCTTGGCATTTGGTTTACCTGCCAGGTGTATAGCAGCAATTG	480
DB	421	CAATGTTTCCATCACTCTCTTGGCATTTGGTTTACCTGCCAGGTGTATAGCAGCAATTG	480
QY	481	TCCAATCTTCATATGAGAACCAAGTAAAGAAAGTTTCCAAATTTGGTGGATTAAGTGAATG	540
DB	481	TCCAATCTTCATATGAGAACCAAGTAAAGAAAGTTTCCAAATTTGGTGGATTAAGTGAATG	540
QY	541	TAAACAAGAAAGCAGTTTGGCTTCTCAAGTTCTTTTGTCTGTACTGCATGCCAATTTATA	600
DB	541	TAAACAAGAAAGCAGTTTGGCTTCTCAAGTTCTTTTGTCTGTACTGCATGCCAATTTATA	600
QY	601	GTCTGTCTTACCCCAATAGAGGGAATCCATACAGATCAAGTTGCTTAAACCTGGGCATATCAAC	660
DB	601	GTCTGTCTTACCCCAATAGAGGGAATCCATACAGATCAAGTTGCTTAAACCTGGGCATATCAAC	660
QY	661	AGGTCCAACAAAATTAAGAAAGATGCTTGATTTGAGCATGATGTTTGGAGATGAGATTT	720
DB	661	AGGTCCAACAAAATTAAGAAAGATGCTTGATTTGAGCATGATGTTTGGAGATGAGATTT	720
QY	721	ATGTGTCTCTGGGAATTTGGGATTTGGCAATACCTGGCTCTGTGGCTGTGACATCTATTC	780
DB	721	ATGTGTCTCTGGGAATTTGGGATTTGGCAATACCTGGCTCTGTGGCTGTGACATCTATTC	780
QY	781	CATCTGTGAGTGAATCTTTTGAATGAGAAATTTTCACTATATTCACAGCAAGCTTAGGAA	840
DB	781	CATCTGTGAGTGAATCTTTTGAATGAGAAATTTTCACTATATTCACAGCAAGCTTAGGAA	840
QY	841	TTGTGTTCCCTTCTAATGAGCAATACAGCATTTGATTTTGGCTGGAAATAGTGAATAG	900
DB	841	TTGTGTTCCCTTCTAATGAGCAATACAGCATTTGATTTTGGCTGGAAATAGTGAATAG	900
QY	901	ATAATAAAACAATTGTATGTGATACATCCCACTTTTATGATAGCTGTTTCTTCCAA	960
DB	901	ATAATAAAACAATTGTATGTGATACATCCCACTTTTATGATAGCTGTTTCTTCCAA	960
QY	961	TTGTGTCTGATATTTTAAAGATATATTTCTGTCATGCTTGAAGAGAAAGTACTGA	1020
DB	961	TTGTGTCTGATATTTTAAAGATATATTTCTGTCATGCTTGAAGAGAAAGTACTGA	1020

Db 961 TTGTTGCTGATATTTAAAGCATATCTTCCTGCGATGCTTGAGAGAAAGATCTGA 1020
Qy 1021 AGATTTAGCATGTTGGGAAGCGTCACAAATTTAAACAACTGAGATATGTTCCAGT 1080
Db 1021 AGATTTAGCATGTTGGGAAGCGTCACAAATTTAAACAACTGAGATATGTTCCAGT 1080
Qy 1081 TGTAGAAATTAAGTTTACACACATTTTGTTCATATTTGATATATTTATATCAACCAACT 1140
Db 1081 TGTAGAAATTAAGTTTACACACATTTTGTTCATATTTGATATATTTATATCAACCAACT 1140
Qy 1141 TCAAGTTTGTATTTGTTAATTAATGATTTATTCAGAGAAAAA 1195
Db 1141 TCAAGTTTGTATTTGTTAATTAATGATTTATTCAGAGAAAAA 1195

RESULT 14
US-10-394-087-35
; Sequence 35, Application US/10394087
; Publication No. US20030194734A1
; GENERAL INFORMATION:
; APPLICANT: Jatkoe, Tim
; TITLE OF INVENTION: SELECTION OF MARKERS
; FILE REFERENCE: CDS 265 US NP
; CURRENT APPLICATION NUMBER: US/10/394,087
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,790
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: human
US-10-394-087-35

Query Match 100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1,1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGAAGCTGACGGTCAAGCTAAGCGGAAGTGGGCTGGAAGCCATCTATTTATAG 60
Db 1 CCGAAGCTGACGGTCAAGCTAAGCGGAAGTGGGCTGGAAGCCATCTATTTATAG 60
Qy 61 AATTAATGGAAGCAAGAAAGACATCAAAACCAAGAGACTTTGGAAATGAAAGCTTA 120
Db 61 AATTAATGGAAGCAAGAAAGACATCAAAACCAAGAGACTTTGGAAATGAAAGCTTA 120
Qy 121 GGAGAAATTTAGAAAGACGATTTATTCATTAAGACACGGAGAGACCAAGATCTTA 180
Db 121 GGAGAAATTTAGAAAGACGATTTATTCATTAAGACACGGAGAGACCAAGATCTTA 180
Qy 181 AAAAGCTGCTTTTGGCATTTGGACCAAGCCATGCTGATGAATTTGACTGCCCTT 240
Db 181 AAAAGCTGCTTTTGGCATTTGGACCAAGCCATGCTGATGAATTTGACTGCCCTT 240
Qy 241 CAGAACTTGAGCACAACAGAACTCTTTCACAGTGGACCTTGCCAAATTAATAGCTG 300
Db 241 CAGAACTTGAGCACAACAGAACTCTTTCACAGTGGACCTTGCCAAATTAATAGCTG 300
Qy 301 CTATTATAGCATCTGACTTTTCTTTACACTCTTCTGAGGGAATTAATTCACCTTTAG 360
Db 301 CTATTATAGCATCTGACTTTTCTTTACACTCTTCTGAGGGAATTAATTCACCTTTAG 360
Qy 361 CAACTTCCCATCAAAATATTTTATTAATTCAGATCCGTCATCAACAAAGCTCTG 420
Db 361 CAACTTCCCATCAAAATATTTTATTAATTCAGATCCGTCATCAACAAAGCTCTG 420
Qy 421 CAATGTTTCCATCACTCTTGGCATTTGCTTACCTGCGAGTGTATAGCAGCAATG 480
Db 421 CAATGTTTCCATCACTCTTGGCATTTGCTTACCTGCGAGTGTATAGCAGCAATG 480
Qy 481 TCCAATTCATTAATGAAACCAAGTATTAAGAGTTTCCACTTGGTGGATTAAGTATGT 540
Db 481 TCCAATTCATTAATGAAACCAAGTATTAAGAGTTTCCACTTGGTGGATTAAGTATGT 540

Db 481 TCCAATTCATTAATGAAACCAAGTATTAAGAGTTTCCACTTGGTGGATTAAGTATGT 540
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Qy 601 GTCTGTCTTACCCCAATGAGGAGATCTTACAGATCAAGTTGCTTAACTGGGCAATCAAC 660
Db 601 GTCTGTCTTACCCCAATGAGGAGATCTTACAGATCAAGTTGCTTAACTGGGCAATCAAC 660
Qy 661 AGGTCCAAACAAATTAAGAAAGATGCTGATTTGAGCATGATGTTTGGAGATGAGATTT 720
Db 661 AGGTCCAAACAAATTAAGAAAGATGCTGATTTGAGCATGATGTTTGGAGATGAGATTT 720
Qy 721 ATGTGTCTTGGAAATTTGGGATTTGGCAATATCTGCTCTGTGGCTGTGACATCTATTC 780
Db 721 ATGTGTCTTGGAAATTTGGGATTTGGCAATATCTGCTCTGTGTGACATCTATTC 780
Qy 781 CATCTGTAGATGATCTTTTGCATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGAG 840
Db 781 CATCTGTAGATGATCTTTTGCATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGAG 840
Qy 841 TTGTTTCCCTCTACTGAGGCAATACAGCATTTGATTTTGCCTGAAATAGTGATAG 900
Db 841 TTGTTTCCCTCTACTGAGGCAATACAGCATTTGATTTTGCCTGAAATAGTGATAG 900
Qy 901 AATATAAAACAAATTTGTATGTATACACCTCCAACTTTTATATAGTCTTTTCTTCCAA 960
Db 901 AATATAAAACAAATTTGTATGTATACACCTCCAACTTTTATATAGTCTTTTCTTCCAA 960
Qy 961 TTGTTGCTCTGATATTTAAAGCATACTATTCCTGCAATGCTTGAGAAAGATACTGA 1020
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RESULT 15
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; Sequence 713, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15

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; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 713
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-713

Query Match      100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1,1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 841 TTGTTCCCTTCTACTGGGCAAAATACGCAATGATTTTGGCTGGAAATGAATGATAG 900
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GenCore version 5.1.6
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Run on: December 6, 2005, 16:30:04 ; Search time 948 Seconds

(without alignments)
2957.088 Million cell updates/sec

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Perfect score: 1790

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Dextop 6.0, Dextext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Published Applications NA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1790	100.0	1177	6	US-10-696-639-15
2	1790	100.0	1193	8	US-10-165-044-1
3	1790	100.0	1193	7	US-10-408-009-1
4	1790	100.0	1193	8	US-10-857-785-1
5	1790	100.0	1193	8	US-10-856-109-1
6	1790	100.0	1193	8	US-10-830-899-2
7	1790	100.0	1193	8	US-10-753-195-1
8	1790	100.0	1193	9	US-10-752-421-1

9	1790	100.0	1193	9	US-10-861-662-2	Sequence 2, Appli
10	1790	100.0	1195	3	US-09-759-143-878	Sequence 878, App
11	1790	100.0	1195	3	US-09-780-669-878	Sequence 878, App
12	1790	100.0	1195	3	US-09-822-827-878	Sequence 878, App
13	1790	100.0	1195	3	US-09-895-793-878	Sequence 878, App
14	1790	100.0	1195	3	US-09-895-814-878	Sequence 878, App
15	1790	100.0	1195	5	US-10-012-896-878	Sequence 878, App
16	1790	100.0	1195	5	US-10-011-095-1	Sequence 1, Appli
17	1790	100.0	1195	5	US-10-010-667A-1	Sequence 1, Appli
18	1790	100.0	1195	5	US-10-205-823-396	Sequence 396, App
19	1790	100.0	1195	6	US-10-144-678A-878	Sequence 878, App
20	1790	100.0	1195	6	US-10-294-025-878	Sequence 878, App
21	1790	100.0	1195	6	US-10-393-550-35	Sequence 35, Appl
22	1790	100.0	1195	6	US-10-393-567-35	Sequence 35, Appl
23	1790	100.0	1195	6	US-10-394-087-35	Sequence 35, Appl
24	1790	100.0	1195	6	US-10-295-027-713	Sequence 713, App
25	1790	100.0	1195	6	US-10-295-027-1130	Sequence 1130, Ap
26	1790	100.0	1195	8	US-10-643-795A-16	Sequence 16, Appl
27	1790	100.0	1195	8	US-10-643-795A-42	Sequence 42, Appl
28	1790	100.0	1195	9	US-10-750-262-1	Sequence 1, Appli
29	1790	100.0	1195	9	US-10-948-518-16	Sequence 16, Appli
30	1790	100.0	1195	9	US-10-948-518-42	Sequence 42, Appli
31	1790	100.0	1195	9	US-10-956-157-1811	Sequence 1811, Ap
32	1790	100.0	1195	9	US-10-956-157-7046	Sequence 7046, Ap
33	1790	100.0	1195	9	US-10-858-887-1	Sequence 1, Appli
34	1790	100.0	1195	9	US-10-631-467-428	Sequence 428, App
35	1790	100.0	1195	10	US-11-051-454-396	Sequence 396, App
36	1790	100.0	1201	7	US-10-425-114-1645	Sequence 1645, A
37	1790	100.0	1277	3	US-09-814-353-19910	Sequence 1910, A
38	1790	100.0	1330	7	US-10-755-889-191	Sequence 191, App
39	1732.5	96.8	1365	8	US-10-830-899-6	Sequence 6, Appli
40	1732.5	96.8	1365	9	US-10-861-662-6	Sequence 6, Appli
41	1724	96.3	1354	8	US-10-723-860-5120	Sequence 5120, Ap
42	1503	84.0	1211	9	US-10-631-467-1300	Sequence 1300, Ap
43	1358.5	75.9	3627	5	US-10-011-095-6	Sequence 6, Appli
44	1358.5	75.9	3627	5	US-10-010-667A-6	Sequence 6, Appli
45	1358.5	75.9	3627	6	US-10-165-044-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-696-639-15
US-10-696-639-15 Application US/10696639
Publication No. US2005007439A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corporation
APPLICANT: Bourrier, Maureen J.
TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
FILE REFERENCE: 01040/1
CURRENT APPLICATION NUMBER: US/10/696,639
CURRENT FILING DATE: 2003-10-29
PRIOR APPLICATION NUMBER: 60/422,176
NUMBER OF SEQ ID NOS: 3114
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 1177
TYPE: DNA
ORGANISM: homo sapiens
US-10-696-639-15

Alignment Scores:
Pred. No.: 1,63e-195
Score: 1790.00
Best Local Similarity: 100.00%
Best Percent Similarity: 100.00%
Query Match: 100.00%
DB: 8
Gaps: 0

US-10-750-262-2 (1-339) x US-10-696-639-15 (1-1177)

Length: 1177
Matches: 339
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

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 Db AATTAGAGAGAGAGATATTGTCATTAAGACACGGGAGAGACAGCATGTCTAAAGAA 185
 QY 41 ProValLeuLeuHisLysLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
 Db CTGTGCTTTGGCATTTGGACCAACAGCCCATGTGAGAAATTTGACTGCCCCCTTCAGAA 245
 QY 61 LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProLysLeuAlaAlaIle 80
 Db CTTCAGACACACAGGAATCTTTCCACAGTGGCACTTCCCAATTAATAGCTGCTATT 305
 QY 81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
 Db ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACT 365
 QY 101 SerHisGlnGlnTyrPheTyrLysIleProLysLeuValIleAsnLysValLeuProMet 120
 Db TCCCATCAACAATATTTTATTAATAATTCACATCTGTCTCATCAACAAGCTTTGCCAATG 425
 QY 121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
 Db GTTTCATCACTCTCTTGGCATTTGCTTACCTGACAGTGTGATACAGCAATGTGCCAA 485
 QY 141 LeuHisAsnGlyThrLysTyrLysLysPheProHisIleThrLeuLysLysTrpMetLeuThr 160
 Db CTTCATTAATGGAACCAAGTATTAAGATTCCACATGTGTGATGAAGTGAATGTTAAACA 545
 QY 161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
 Db AGAAGCAGATTTGGCTTCTCAGATTTCTTTTGTGCTGACTGCAATGCAATTTATAGCTTG 605
 QY 181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
 Db TCTTACCCAAATGAGCGCATCTTACAGATACAGTGTCTAACTGGCATTCACAGCTC 665
 QY 201 GlnGlnAsnLysGluAspAlaTrpIleGlnHisAspValTrpArgMetGluIleTyrVal 220
 Db CAAACAAATTAAGAAAGATGCTGCTGATTCAGCATGATTTTGAGAAATGAGATTTATGTG 725
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 Db TCTCTGGGAATTTGGGATTTGGCAATCTGCTGCTGTGGCTGAGCATTTATTCACATCT 785
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 Db GTGAGTACTCTTGGACATGGAGAAATTTCACTATATTCAGACCAAGCTTAGGAATGTG 845
 QY 261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
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 QY 281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
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 QY 301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
 Db GTCCGATATTTTAAAGCATCTATCTCTCCACTCTTGAAGAGAAATATCTGAAGATT 1025
 QY 321 ArgHisGlyTyrGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
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RESULT 2
 US-10-165-044-1
 ; Sequence 1, Application US/10165044
 ; Publication No. US20030149531A1
 ; GENERAL INFORMATION:

/ APPLICANT: Agensys, Inc.
 / APPLICANT: Rene S. Hubert
 / APPLICANT: Arthur B. Raitano
 / APPLICANT: Douglas Safiran
 / APPLICANT: Daniel E.H. Afar
 / APPLICANT: Steven Chappel Mitchell
 / APPLICANT: Mary Faris
 / APPLICANT: Aya Jakobovits
 / TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
 / TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
 / FILE REFERENCE: 51158-20016.02
 / CURRENT APPLICATION NUMBER: US/10/165,044
 / PRIOR APPLICATION NUMBER: US 60/087,520
 / PRIOR FILING DATE: 1998-06-01
 / PRIOR APPLICATION NUMBER: US 60/091,183
 / PRIOR FILING DATE: 1998-06-30
 / PRIOR APPLICATION NUMBER: US 09/323,873
 / PRIOR FILING DATE: 1999-06-01
 / PRIOR APPLICATION NUMBER: US 09/455,486
 / PRIOR FILING DATE: 1999-12-06
 / PRIOR APPLICATION NUMBER: WO 99/62941
 / PRIOR FILING DATE: 1999-06-01
 / PRIOR APPLICATION NUMBER: PCT/US00/33040
 / PRIOR FILING DATE: 2000-12-06
 / NUMBER OF SEQ ID NOS: 57
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 1
 / LENGTH: 1193
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (64)...(1191)
 / US-10-165-044-1
 / US-10-750-262-2 (1-339) x US-10-165-044-1 (1-1193)
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

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QY 141 LeuH1aSnG1YThrIlySTYlySLySPheProH1eSTrpleuAbspLySTrPMeLleuThr 160
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 QY 201 GlnGlnAsnLySGlnuAspAlaTrpIleGlnH1aAspValTrpArgMetGluIleTyVal 220
 Db 664 CAACAAATAAAGAAGATGCTCGATTTGAGCATGATTTGGAGAAATGAGATTTATGTG 723
 QY 221 SerLeuGlyIleValGlyLeuAlaIleuAlaLeuAlaValThrSerIleProSer 240
 Db 724 TCTCGGGAATGTGGGATTTGGCAATACAGCTGCTGTGGCTGAGCATCTTCCATCT 783
 QY 241 ValSerAspSerLeuThrTrpArgGlnPheH1eTyTrpIleGlnSerLySLeuglyIleVal 260
 Db 784 GTGAGTGACTCTTGAACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGAGAAATGTT 843
 QY 261 SerLeuLeuLeuGlyThrIleH1aIleuIlePheAlaTrpAsnLySTrIleAspIle 280
 Db 844 TCCCTTACTGCGGACAAATACACCATTTGATTTTGCCTGGAAATAGTGAATAGTAA 903
 QY 281 LySGlnPheValTrpTyThrProProThrPheMetIleAlaValPheLeuProIleVal 300
 Db 904 AAACAATTTGATGGTATACACCTCACTTTATGATAGCTGTTTCTTCCATTGTT 963
 QY 301 ValIleuIlePheLySerIleLeuPheLeuProCysLeuAlySLyIleLeuLySle 320
 Db 964 GTCTGATATTTAAAGCATACTATCTCGCATGCTTGAGAGAAAGATATCTGAAGATT 1023
 QY 321 ArgH1aGlyTrpGluAspValThrLySleAsnLySThrGluIleCysSerGlnLeu 339
 Db 1024 AGACATGGTTGGAAAGAGCTCAACCAAAATTAACAAACTGAGATATGTTCCAGTTG 1080
 RESULT 3
 US-10-408-009-1
 ; Sequence 1, Application US/10408009
 ; Publication No. US20040072196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Daniel E. Afar
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Douglas C. Saffran
 ; APPLICANT: Stephen C. Mitchell
 ; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
 ; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
 ; FILE REFERENCE: 511582001603
 ; CURRENT APPLICATION NUMBER: US/10/408,009
 ; PRIOR FILING DATE: 2003-04-04
 ; PRIOR APPLICATION NUMBER: 09/455,486
 ; PRIOR FILING DATE: 1999-12-06
 ; PRIOR APPLICATION NUMBER: 09/323,873
 ; PRIOR FILING DATE: 1999-06-01
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1193
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (64)...(1083)
 US-10-408-009-1
 Alignment Scores: 1.66e-195 Length: 1193
 Pred. No.:

Score: 1790.00 Matches: 339
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0
 US-10-750-262-2 (1-339) x US-10-408-009-1 (1-1193)
 QY 1 MetGluSerArgLyAspIleThrAsnGlnGlnLeuTrpLyMetLyProArgArg 20
 Db 64 ATGGAAGAGAAAAGACATCAACAAAGAGAACTTTGGAAATAGAGCTTGGAGA 123
 QY 21 AsnLeuGlnGluAspAspTyIleuH1aLyAspThrGlyIleuThrSerMetLeuLyArg 40
 Db 124 AATTGAGAAGAGCATTTATTTGCATAGAGACAGGAGAGACACGATGTAAGAAAAGA 183
 QY 41 ProValIleuLeuH1aSnG1ThrAlaH1aIleuAlaAspGlnPheAspCysProSerGlu 60
 Db 184 CTTGTGCTTTTGCAATTTGACACCAACAGCCATGCTGATGAATTTGACCTGCCCTTACAGA 243
 QY 61 LeuGlnH1aSnGlnGlnLeuPheProGlnTrpH1aSerProIleLyIleAlaIle 80
 Db 244 CTTGAGACACACAGAACTTTTCCACAGTGGCATTTGCCAATTAATAGCTGCTATTT 303
 QY 81 IleAlaSerLeuThrPheLeuTyThrIleuLeuArgGlnValIleH1aProLeuAlaThr 100
 Db 304 ATACATCTCTGACCTTTCTTACACTCTTGAAGGAAATATTCACCTTTAGCAACT 363
 QY 101 SerH1aGlnGlnTyRheTyLySleProIleLeuValIleAsnLyValLeuProMet 120
 Db 364 TCCCATCAACAATATTTTAAATTCACATCTGTGATCAACAAAGCTTCCCAATG 423
 QY 121 ValSerIleThrLeuLeuAlaLeuValTyIleuProGlyValIleAlaIleValGln 140
 Db 424 GTTTCATCACTCTCTGGCATTTGTTTACTCTGCAGGTGTGATAGCAATTTGCTCAA 483
 QY 141 LeuH1aSnG1YThrIlySTYlySLySPheProH1eSTrpleuAbspLySTrPMeLleuThr 160
 Db 484 CTTCAATAATGAACCAAGTATAAGAGTTCCACATTGGTGGATAGTGAAGCTTTAACA 543
 QY 161 ArgLySGlnPheGlyLeuLeuSerPhePheAlaValIleuH1aIleTySerLeu 180
 Db 544 AGAAACAGTGTGGGCTTCACAGTTCTTTTGTGTGCTGATGCATCAATTATACCTG 603
 QY 181 SerTyPProMetArgArgSerTyArgTyTyLySLeuleuAenTPraIaTyGlnGlnVal 200
 Db 604 TCTTACCCATGAGGCGGATCTCAAGATACAGATTCTAAACGGGCATATCAACAGCTC 663
 QY 201 GlnGlnAsnLySGlnuAspAlaTrpIleGlnH1aAspValTrpArgMetGluIleTyVal 220
 Db 664 CAACAAATAAAGAAGATGCTCGATTTGAGCATGATTTGGAGAAATGAGATTTATGTG 723
 QY 221 SerLeuGlyIleValGlyLeuAlaIleuAlaLeuAlaValThrSerIleProSer 240
 Db 724 TCTCGGGAATGTGGGATTTGGCAATACAGCTGCTGTGGCTGAGCATCTTCCATCT 783
 QY 241 ValSerAspSerLeuThrTrpArgGlnPheH1eTyTrpIleGlnSerLySLeuglyIleVal 260
 Db 784 GTGAGTGACTCTTGAACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGAGAAATGTT 843
 QY 261 SerLeuLeuLeuGlyThrIleH1aIleuIlePheAlaTrpAsnLySTrIleAspIle 280
 Db 844 TCCCTTACTGCGGACAAATACACCATTTGATTTTGCCTGGAAATAGTGAATAGTAA 903
 QY 281 LySGlnPheValTrpTyThrProProThrPheMetIleAlaValPheLeuProIleVal 300
 Db 904 AAACAATTTGATGGTATACACCTCACTTTATGATAGCTGTTTCTTCCATTGTT 963
 QY 301 ValIleuIlePheLySerIleLeuPheLeuProCysLeuAlySLyIleLeuLySle 320
 Db 964 GTCTGATATTTAAAGCATACTATCTCGCATGCTTGAGAGAAAGATATCTGAAGATT 1023
 QY 321 ArgH1aGlyTrpGluAspValThrLySleAsnLySThrGluIleCysSerGlnLeu 339

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Db      1024 AGACATGTTGGGAAGAGCTACCCAAATTAACAAACTGAGATATGTTCCAGTTG 1080
|||||
RESULT 4
US-10-857-785-1
; Sequence 1, Application US/10857785
; Publication No. US20040219162A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 511582001607
; CURRENT APPLICATION NUMBER: US/10/857,785
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)
US-10-857-785-1

Alignment Scores:
Pred. No.:      1.66e-195      Length:      1193
Score:          1790.00      Matches:      339
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:               Gaps:      0

US-10-750-262-2 (1-339) x US-10-857-785-1 (1-1193)
QY      1 MetGluSerArgLysAspIleThrAsnGlnGluLeuTrpLysMetLysProArgArg 20
Db      64 ATGGAAGCAAGAAAGACATCACAAACCAAGAAAGAACTTTGGAAATGAAGCCTTAGAGAGA 123
QY      21 AsnLeuGluLysAspArgTrpLeuHisLysAspThrGlyGlnTrpSerMetLeuLysArg 40
Db      124 AATTGAGAGAGAGCGATTATTTCATTAAGGACAGGAGAGACGACAGCATGCTAAGAAAGA 183
QY      41 ProValLeuLeuHisLysGlnThrAlaHisAlaAspGluPheAspCysProSerGln 60
Db      184 CCGTGTGCTTTTGCAATTGGACCAAAACGCCATGCTGAATGAATTTGACTGCCCTTCAGAA 243
QY      61 LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
Db      244 CTTAGACACACACAGAACTTTTCCACAGTGGCACTTGCCAAATTAATAATAGCTGATAT 303
QY      81 IleAlaSerLeuThrPheLeuTrpThrLeuLeuArgGluValIleHisProLeuAlaThr 100
Db      304 ATAGCATCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTTAGCAACT 363
QY      101 SerIleGlnIleTrpPheTrpLysIleProIleLeuValIleAsnLysValLeuProMet 120
Db      364 TCCCATCAACAATATTTTATTAATAATTCCAATCTGGGTCATCAACAAGCTCTGGCAATG 423
QY      121 ValSerIleThrLeuAlaLeuValTrpLeuProGlnValIleAlaAlaIleValGln 140
|||||
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Db      424 GTTTCATCACTCTCTGGCAGTTGTTTACTGCTGCCAGGTGTGATAGACGAATTTGCCAA 483
QY      141 LeuHisAsnGlyThrLysTrpLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
Db      484 CTTCAATATGGAACCAAGATATMAAGATTTCCACATTTGGATTGATTAAGTGAATGTTAA 543
QY      161 ArgLysGlnPheGlyLeuLeuSerPhePheHisAlaValLeuHisAlaIleTrpSerLeu 180
Db      544 AGAAAGCATTTGGGCTTCTCAAGTTCTTTTCTGTCAGTCATGCAATTTATAGTCTG 603
QY      181 SerTrpProMetArgArgSerTrpArgTrpLysLeuLeuAsnTrpAlaTrpGlnGlnVal 200
Db      604 TCTTATCCCAATGAGGCGATCTTACAGATATCAAGTTGGCTMAACTGGGCAATATCAACAGG 663
QY      201 GlnGlnAsnLysGluAspAlaTrpIleGlnHisAspValTrpArgMetGlnIleTrpVal 220
Db      664 CAACAAATTAAGAAAGAGCTGAGATTGAGATGATGTTGGAGAAATGCAATTTATGCTG 723
QY      221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuAlaValThrSerIleProSer 240
Db      724 TCTCTGGGAATTTGGGATTTGGCAATTAAGTCTGCTGTTGGCTGTACATTAATTCATCT 783
QY      241 ValSerAspSerLeuThrTrpArgGluPheHisTrpIleGlnSerLysLeuGlyIleVal 260
Db      784 GTGAGTGACTCTTTGACATGAGAGAAATTTCACTATTATTCAGACGCAAGCTAGAAATTT 843
QY      261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
Db      844 TCCCTTCTACTGGGCAACAATACACGCAATGATTTTGTCTGGAAATGATGATATATA 903
QY      281 LysGlnPheValTrpTrpThrProProThrPheMetIleAlaValPheLeuProIleVal 300
Db      904 AAACAAATTTGATGGTATACCTTCCACTTATTAATGATAGCTGTTTCCCTCAATGTTT 963
QY      301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
Db      964 GTCCGTGATATTTAAAGCATATCTATTCCTGCGCATGCTTGAGGAAGAAATGATGAAGAT 1023
QY      321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGlnIleCysSerGlnLeu 339
Db      1024 AGACATGTTGGGAAGAGCTACCCAAATTAACAAACTGAGATATGTTCCAGTTG 1080
|||||

RESULT 5
US-10-856-109-1
; Sequence 1, Application US/10856109
; Publication No. US20040219591A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 511582001606
; CURRENT APPLICATION NUMBER: US/10/856,109
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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LOCATION: (64) ... (1083)
US-10-856-109-1

Alignment Scores:
Pred. No.: 1,666-195 Length: 1193
Score: 1790.00 Matches: 339
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-750-262-2 (1-339) x US-10-856-109-1 (1-1193)

QY 1 MetGluSerArgLysAspIleThrAsnGlnGluLeuTrpLysMetLysProArg 20
DB 64 ATGGAAGAGAAAAGACATCAACAAAGAACTTGGAAATGAACTTGGAGAA 123
QY 21 AsnLeuGluLysAspTrpLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
DB 124 AATTAGAAAGAGACATTAATTGCAATAAGACACGGGAGAGACAGCATGCTAAAGAA 183
QY 41 ProValLeuLeuHisLysGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
DB 184 CTGTGCTTTGGCATTTGCACTCAACCAAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243
QY 61 LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLysProIleLysIleAlaIle 80
DB 244 CTTAGGACACACAGGAATCTTTCCACAGTGGCATTTGCCAATTAAATAGCTCTATT 303
QY 81 IleAlaSerLeuThrPheLeuTrpThrLeuLeuArgGluValIleHisProLeuAlaThr 100
DB 304 ATACATCTCTGACTTTCTTTACACTCTTCGAGGAGAAATTCACCTTACACT 363
QY 101 SerIleGlnGlnTrpPheTrpLysIleProIleLeuValIleAsnLysValLeuProMet 120
DB 364 TCCCATCAACAATATTTTATTAATTCATCCGTCATCAACAAGTCTTGGCAATG 423
QY 121 ValSerIleThrLeuLeuAlaLeuValTrpLeuProGlyValIleAlaIleValGln 140
DB 424 GTTTCATCACTCTCTTGGCATTTGGTTTACCTGCCAGGTGATGACGCAATGTCGAA 483
QY 141 LeuHisAsnGlyThrLysTrpLysLysAspProHisTrpLeuAspLysTrpMetLeuThr 160
DB 484 CTTTCATATGGAACCAAGTATTAAGAGTTTCCACATTTGGTGAATAGTGAATTAACA 543
QY 161 ArgLysGlnPheGlyLeuLeuSerPhePheAlaValLeuHisAlaIleTrpSerLeu 180
DB 544 AGAAGAGAGTTTGCGCTTCCAGTTTCTTTTTCCTGACTGCAATTAATTAAGTCTG 603
QY 181 SerTrpProMetArgTrpSerTrpArgTrpLysLeuLeuAsnTrpAlaTrpGlnGlnVal 200
DB 604 TCTTACCATGAGGCAATCTTACAGATTAAGTTGCTAACTGGGCAATTCACAGGTC 663
QY 201 GlnGlnAsnLysGluAspAlaTrpIleGlnHisAspValTrpArgMetGluIleTrpVal 220
DB 664 CAACAATAATTAAGAAAGATGCTGATTTGACATGATGTTTGGAGAAATGAGATTAAGT 723
QY 221 SerLeuGlyLysValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
DB 724 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGACATCTAATTCATCT 783
QY 241 ValSerAspSerLeuThrTrpArgGluPheHisTrpTrpIleGlnSerLysLeuGlyIleVal 260
DB 784 GTGAGGACCTTTGACATGAGAGAAATTTCACTAATTAAGAGCAAGCTAAGAAATTTGTT 843
QY 261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
DB 844 TCCCTTCTAGTGGCAATACAGCATTAATTTTGGCTGGAAATAGTGAATAGATATA 903
QY 281 LysGlnPheValTrpTrpThrProProThrPheMetIleAlaValPheLeuProIleVal 300
DB 904 AAACAATTTGTATGATATACCTCAACTTTATATAGTGTGTTTCTTCCATTTGTT 963

QY 301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysIleLeuLysIle 320
DB 964 GTTCTGATATTTTAAAGCACTACTATTTCCGTCATGCTTGGAGAGAAAGATTCGAAGATT 1023
QY 321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
DB 1024 AACATGTTGGTGGGAAGACCTCAACAAATTAACAATACTGAGATATGTTCCAGTTG 1080

RESULT 6

US-10-830-899-2
Sequence 2, Application US/10830899
Publication No. US20040253232A1
GENERAL INFORMATION:

APPLICANT: Jakobovits, Aya
APPLICANT: Etesami, Soudabeh
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Perez-Villar, Juan
APPLICANT: Meyrick Morrison, Karen Jane
APPLICANT: Jia, Xiao-Chi
APPLICANT: Faris, Mary
APPLICANT: Gudas, Jean
APPLICANT: Raitano, Arthur B.
TITLE OF INVENTION: Antibodies and Molecules Derived
FILE REFERENCE: 51158-20016.26
CURRENT APPLICATION NUMBER: US/10/830, 899
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: 09/323, 873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 10/010, 667
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 10/011, 095
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 10/236, 878
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/455, 486
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 60/091, 183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 103
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2

LENGTH: 1193
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (66) ... (1085)
US-10-830-899-2

Alignment Scores:
Pred. No.: 1,666-195 Length: 1193
Score: 1790.00 Matches: 339
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-750-262-2 (1-339) x US-10-830-899-2 (1-1193)

QY 1 MetGluSerArgLysAspIleThrAsnGlnGluLeuTrpLysMetLysProArg 20
DB 66 ATGGAAGAGAAAAGACATCAACAAAGAACTTGGAAATGAACTTGGAGAA 125
QY 21 AsnLeuGluLysAspTrpLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
DB 126 AATTAGAAAGAGACATTAATTGCAATAAGACACGGGAGAGACAGCATGCTAAAGAA 185
QY 41 ProValLeuLeuHisLysGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
DB 186 CTGTGCTTTGGCATTTGCACTCAACCAAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245
QY 61 LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLysProIleLysIleAlaIle 80

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Db      246 CTTGACGACACAGAGAACTTTTCCACAGTGGCACTTGCCAAATTAATAGCTGTAAT 305
Qy      81  ILeAlaSerLeuThrPheLeuTyThrLeuLeuAArgGluValIleHisProLeuAlaThr 100
Db      306 ATAGATCTCTGACCTTTCTTTACACTCTTCTGAGAGAAAGTAATTCACCCCTTTAGCAACT 365
Qy      101 SerHisGlnGlnTyPheTyTyIleProIleLeuValIleAsnLysValLeuProMet 120
Db      366 TCCCATCAACAATATTTTATTAATAATCCAAATCTGGTCATACAAAGCTTTGGCCAAATG 425
Qy      121 ValSerIleThrLeuLeuAlaLeuValTyLeuProGluValIleAlaAlaIleValGln 140
Db      426 GTTTCATCATCTCTCTTGGCACTTGTTTACCTGCCAGGTGATAGCAATTTGCCAA 485
Qy      141 LeuHisAsnGlyThrLysTyTyLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
Db      486 CTTCAATATGGAACCAAGATATAAGAAATTTCCACATGGTGATGATAGTGTATTAACA 545
Qy      161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTySerLeu 180
Db      546 AGAAAGCAGTTGGGCTTCTCAGTTCTTTTGGCTGATGCAATTTATAGTCTG 605
Qy      181 SerTyTrpMetArgArgSerTyArgTyTyLysLeuLeuAsnTrpAlaTyGlnGlnVal 200
Db      606 TCTTACCCAAATAGGCGCATCTTACATACATCAAGTTGCTAACTGGGCATATCAACAGCTC 665
Qy      201 GlnGlnAsnLysGluAspAlaTrpIleGlnHisAspValTrpArgMetGluIleTyVal 220
Db      666 CAACAAATATTAAGAAATGCTGATTTGAGCATGATGTTTGGAAATGAGATTTATGTG 725
Qy      221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
Db      726 TCTCTGGGAATTTGGGATTTGGCAATTAAGTGGCTGTGTTGGCTGATCATTTATTCATCT 785
Qy      241 ValSerAspSerLeuThrTrpArgGluPheHisTyTrIleGlnSerLysLeuGlyIleVal 260
Db      786 GTAGAGTACTCTTGACATGAGAGAAATTTCACTATATTCCAGCAAGCTAGGAATGTT 845
Qy      261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
Db      846 TCCCTTCTACTGGGCAACATACAGCATGATTTTCTGCGAATAAGTGAATGAGATTA 905
Qy      281 LysGlnPheValTrpTyThrProProThrPheMetIleAlaValPheLeuProIleVal 300
Db      906 AAACAAATTTGATAGTATACCTCCCACTTTATGATAGTGTGTTTCTCTCCAAATGTT 965
Qy      301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysIleLeuLysIle 320
Db      966 GTCTGATATTTTAAAGCATACTATTTCTGCAATGCTTGAAGAAAGATAGTGAAGATT 1025
Qy      321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
Db      1026 AGACATGTTGGGAAGAGCTCACCAAAATTAACAAAACGTAGATATGTTCCAGATTG 1082

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; PRIOR APPLICATION NUMBER: US/10/165,044
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: WO 99/62941
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/US00/33040
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1191)
; US-10-753-195-1

Alignment Scores:
Pred. No.: 1,666-195 Length: 1,193
Score: 1790.00 Matches: 339
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 8

US-10-750-262-2 (1-339) x US-10-753-195-1 (1-1193)
Qy      1 MetGluSerArgLysAspIleThrAsnGlnGluLeuTrpLysMetLysProArg 20
Db      64 ATGGAAGCAGAAAGACATTCACAAACCAAGAAAGAACTTTGAAATGAAGCTAGAGAA 123
Qy      21 AsnLeuGluGluAspAspTyLeuHisLysAspThrGlyGlnThrSerMetLeuLysArg 40
Db      124 AATTTGAAGAGAGACATTTATTTGATTAAGACACACGGAGAGACCGCATGCTTAATAAGA 183
Qy      41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
Db      184 CTGTGCTTTGGCATTTGGACCAACAGCCGATGATGAATTAAGTCCCTTACGAA 243
Qy      61 LeuGlnHisThrGlnGlnLeuPheProGlnTrpHisLeuProIleLysIleAlaIle 80
Db      244 CTTGACGACACAGAGAACTTTTCCACAGTGGCACTTGCCAAATTAATAGCTGTAAT 303
Qy      81  ILeAlaSerLeuThrPheLeuTyThrLeuLeuAArgGluValIleHisProLeuAlaThr 100
Db      304 ATAGATCTCTGACCTTTCTTTACACTCTTCTGAGAGAAAGTAATTCACCCCTTTAGCAACT 363
Qy      101 SerHisGlnGlnTyPheTyTyIleProIleLeuValIleAsnLysValLeuProMet 120
Db      364 TCCCATCAACAATATTTTATTAATAATCCAAATCTGGTCATACAAAGCTTTGGCCAAATG 423
Qy      121 ValSerIleThrLeuLeuAlaLeuValTyLeuProGluValIleAlaAlaIleValGln 140
Db      424 GTTTCATCATCTCTCTTGGCACTTGTTTACCTGCCAGGTGATAGCAAGATTTGCCAA 483
Qy      141 LeuHisAsnGlyThrLysTyTyLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
Db      484 CTTCAATATGGAACCAAGATATAAGAAATTTCCACATGGTGATGATAGTGTATTAACA 543
Qy      161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTySerLeu 180
Db      544 AGAAAGCAGTTGGGCTTCTCAGTTCTTTTGGCTGATGCAATTTATAGTCTG 603
Qy      181 SerTyTrpMetArgArgSerTyArgTyTyLysLeuLeuAsnTrpAlaTyGlnGlnVal 200

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US-10-750-262-2 (1-339) x US-10-752-421-1 (1-1193)

QY	1	MetGluSerArgIysAspIleIethAsnGlnGluLeuTrpIysMetLysProArgArg	20
Db	64	ATGAAAGACGAAAGAAAGCATCACAAACCAAGAAAGACTTTGGAAATATGAAGCTTAGGAGA	122
QY	21	AsnLeuGlnGluSerAspTrpIleuHisLysAspThrGlyGluThrSerMetLeuLysArg	40
Db	124	AAATTAAAGAAAGACGATTATTTGGATTAAAGAACACGGGAAGACCGACGATCTAAAGAAAGA	183
QY	41	ProValLeuLeuHisIleuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu	60
Db	184	CTGTGCTTTTGGATTTGGATTTGGACCAAAACAGCCCAAGCTGATGATATTGACCTGCCCTTCAAGAA	243
QY	61	LeuGlnHisThrGlnGluLeuPheProGlnTrpHisIleuProIleLysIleAlaAlaIle	80
Db	244	CTTCAGACACACAGGAACCTTTCCACAGTGGCACTTGGCATTTAAATATAGCTGCTATT	303
QY	81	IleAlaSerLeuThrPheLeuTrpTrpIleuLysArgGluValIleHisProLeuAlaThr	100
Db	304	ATAGCATCTCTGACTTTCTTTTACACTCTTGTGAGGAAAGTAATTCACCTTTAGCAACCT	363
QY	101	SerHisGlnGlnTrpPheTrpLysIleProIleLeuValIleAsnLysValLeuPromet	120
Db	364	TCCCATCAACAATATTTTATATAAATTCACATCTCGTATCAACAAGCTTTGGCCAAATG	423
QY	121	ValSerIleThrLeuLeuAlaLeuValTrpLeuProGlyValIleAlaAlaIleValGln	140
Db	424	GTTCATCATACCTCTCTGGCATTTGGTTTTCCTGCCAGGTGATATGACACCAATTTGCCAA	483
QY	141	LeuHisAsnGlyTrpHisTrpLysLysPheProHisTrpLeuAspLysTrpMetLeuThr	160
Db	484	CTTCATATATGGAACCAAGTATTAAGAACTTTCCACATGTTGATTAAGTGAGTATTTAAACA	543
QY	161	ArgLysGlnPheGlyLeuLeuSerPhePheAlaValLeuHisAlaIleTrpSerLeu	180
Db	544	AGAAAGCAGTTTGGGCTCTCAGTTTCTTTTGGCTGATCTGCATGCAATTTATAGTCTG	603
QY	181	SerTrpPrometArgArgSerTrpArgTrpLysLeuLeuAsnTrpAlaTrpGlnGlnVal	200
Db	604	TCTTACCCATATAGGCGATCTTACAGATACAAAGTTGGCTAAATCGGACATATACAGAGCTC	663
QY	201	GlnGlnAsnLysGluAspAlaTrpIleGlnHisAspValTrpArgMetGluIleTrpVal	220
Db	664	CAACAAATATTAAGAAAGATGCTCGATTTAGCATGATGTTTGGACAAATGAGAACTTTATGTG	723
QY	221	SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer	240
Db	724	TCTCTGGGAAATTTGGGATTTGGCAATATCTGGCTCTGTTGGCTGATCATTTATTCACCT	783
QY	241	ValSerAspSerLeuThrTrpArgGluPheHisGlyTrpIleGlnSerLysLeuGlyIleVal	260
Db	784	GTTAGATGACTCTTTTGCATGGAAGAAATTTCACTATATTTACAGCAACACTGGAATTTGTT	843
QY	261	SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle	280
Db	844	TCCCTTCTACCTGGGCAACAATACAGCATGATTTTTCCTCGGAATAGATGATGATATTA	903
QY	281	LysGlnPheValTrpTrpTrpProThrPheMetIleAlaValIleLeuProIleVal	300
Db	904	AAACAAATTTGATGATGATACACCTCCAACTTTTATGATAGCTGTTTCTTCCCAATGTT	963
QY	301	ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysIleLeuLysIle	320
Db	964	GTCCTGATATTTTAAAGCATATCTATTTCTCTGCAAGCTTGGAGAAAGATATCTAAAGATT	1023
QY	321	ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu	339
Db	1024	AGACATGTTGGGAAGACGTACCAAAATTTACAAAACCTAGATATGTTCCAGATTG	1080

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GENERAL INFORMATION:
APPLICANT: Jakobovits, Aya
APPLICANT: Etesseant, Soudabeh
APPLICANT: Chaillita-Bid, Pia M.
APPLICANT: Perez-Villat, Juan
APPLICANT: Meyrick Morrison, Karen Jane
APPLICANT: Jia, Xiao-Chi
APPLICANT: Paris, Mary
APPLICANT: Gudas, Jean
APPLICANT: Raitano, Arthur B.
TITLE OF INVENTION: Antibodies and Molecules Derived
TITLE OF INVENTION: Chereform that Bind to STEAP-1 Proteins
FILE REFERENCE: 51158-20016.26
CURRENT APPLICATION NUMBER: US/10/861,662
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 10/010,667
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 10/011,095
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 10/236,878
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 103
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1193
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (66)...(1085)
US-10-861-662-2

Alignment Scores:
Pred. No.: 1,66e-195 Length: 1193
Score: 1790.00 Matches: 339
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-750-262-2 (1-339) x US-10-861-662-2 (1-1193)
QY 1 MetGluSerArgLysAspIleThrAsnGlnGluLeuTrpLysMetLysProArgArg 20
DB 66 ATGGAAGACAGAAAGACATACAAACAGAGAACTTTGGAATAAGAGCTAGAGAGA 125
QY 21 AsnLeuGlnGluAspAspTrpLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
DB 126 AATTGAGAGAGAGAGATTTATTTGCATTAAGACACGGAGAGACACGACATGCTAAAGA 185
QY 41 ProValLeuLeuHisLysHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
DB 41 PTTGCTTTTGGATTGTCACCAACAGCCCATGCTGATGAATTTGACTGCCCTTGAGAA 245
QY 186 CCGTGCTTTTGGATTGTCACCAACAGCCCATGCTGATGAATTTGACTGCCCTTGAGAA 245
DB 61 LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
DB 246 CTTGAGACACACAGAGAACTTTTCCACAGTGGGACCTTGCAATTAATAATGCTGCTATT 305
QY 81 IleAlaSerLeuThrPheLeuTrpThrLeuLeuArgLysValIleHisProLeuAlaThr 100
DB 306 ATACATCTCTGACTTTTCTTTACACTCTCTCTGAGGAGAAATTCACCTTTTGGCAACT 365
QY 101 SerHisGlnGlnTrpPheTrpLysIleProIleLeuValIleAsnLysValLeuProMet 120
DB 366 TCCCATCAACATATTTTATTAATAATTCCAATCCGTGTCATCACAAAGCTCTTGCAATG 425
QY 121 ValSerIleThrLeuLeuAlaLeuValTrpLeuProGlnValIleAlaAlaIleValGln 140
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DB 426 GTTTCATCACTCTCTTGCACTTGTTTACCTGCAAGTGTAGAGCAATGTCCAA 485
QY 141 LeuHisAsnGlyThrLysLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
DB 486 CTTCATATAGGAACCAAGATTAAGAAAGTTTCCACATGTTGGATGAAGTATGTAAACA 545
QY 161 ArgLysGlnPheGlyLeuLeuSerPhePheAlaValLeuHisAlaIleLysSerLeu 180
DB 546 AGAAAGCAGTTGGAGCTTCAAGTTTCTTTTTCCTGTCATGCATGCATTAATTAAGTCTG 605
QY 181 SerTrpProMetArgArgSerTrpArgTrpLysLeuLeuAsnTrpAlaTrpGlnGlnVal 200
DB 606 TCTTATCCCAATGAGGCGCATCTTACAGATACAAAGTTGCTAACTGGGCAATCAACAGCTC 665
QY 201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTrpVal 220
DB 666 CAACAAATTAAGAAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 725
QY 221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuAlaValThrSerIleProSer 240
DB 726 TCTCTGGGAATTTGGGATTTGGCATTTCTGCTCTGTTGGCTGTGACATCTTATTCATCT 785
QY 241 ValSerAspSerLeuThrTrpArgGluPheHisTrpIleGlnSerLysLeuGlyIleVal 260
DB 786 GTGAGTACTCTTTGACATGAGAGAAATTTACATATTTACAGACAGCAAGCTAGAAATGTT 845
QY 261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
DB 846 TCCCTTCTACTGGGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATG 905
QY 281 LysGlnPheValTrpTrpThrProProThrPheMetIleAlaValPheLeuProIleVal 300
DB 906 AAACAAATTTGATGATGATACCTCCAACTTTATGATGATGATGATGATGATGATGATG 965
QY 301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
DB 966 GTCTGATATTTTAAAGCATATCTATTCCTGCCATGCTTGAAGAGAGATGATGAAGATT 1025
QY 321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGlnIleCysSerGlnLeu 339
DB 1026 AGCATGTTGGGAGAGAGCTGACCAAAATTAACAAATGAGATATGTTCCAGTTG 1082

RESULT 10
US-09-759-143-878
; Sequence 878, Application US/09759143
; Patent No. US2002022248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kaloos, Michael D.
APPLICANT: Renger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 878
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Db	906	AAACAATTGTATGATATACACCTCCAACTTTATATGATAGCTGTTTCCCTCAATTTGTT	965
Qy	301	ValleuilePheylsSerilleuPheleuProCysleuArgylsyleleuysille	320
Db	966	GTCCTGATATTAAAGACATACATATTCCTGCATGCTTGAGGAAGAAGATACGAAGATT	1020
Qy	321	ArxHG1YTrpGluAspValThrIysIleAsnIyThGluIleCysSerGlnIleu	339
Db	1026	AGCAATGGTGTGGGAAGACGTCACCAAAATTTAACMAAATGAGATATGTTCCCGAGTTG	1082
RESULT 11			
US-09-780-669-878			
; Sequence 878, Application US/09780669			
; Patent No. US20020051977A1			
GENERAL INFORMATION:			
APPLICANT: Xu, Jiangchun			
APPLICANT: Dillon, Davin C.			
APPLICANT: Mitcham, Jennifer L.			
APPLICANT: Harlocke, Susan L.			
APPLICANT: Jiang, Yugu			
APPLICANT: Henderson, Robert A.			
APPLICANT: Kalos, Michael D.			
APPLICANT: Fanger, Gary R.			
APPLICANT: Retter, Marc W.			
APPLICANT: Stolk, John A.			
APPLICANT: Day, Craig H.			
APPLICANT: Vedvick, Thomas S.			
APPLICANT: Carter, Darrick			
APPLICANT: Li, Samuel			
APPLICANT: Wang, Aijun			
APPLICANT: Skeiky, Yasir A.W.			
APPLICANT: Hepler, William			
APPLICANT: Hurst, John			
APPLICANT: McNeill, Patricia D.			
APPLICANT: Houghton, Raymond L.			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
FILE REFERENCE: 210121.427C24			
CURRENT APPLICATION NUMBER: US/09/780,669			
CURRENT FILING DATE: 2001-02-09			
NUMBER OF SEQ ID NOS: 943			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 878			
; LENGTH: 1195			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-780-669-878			
Alignment Scores:			
Pred. No.: 1.67e-195 Length: 1195			
Score: 1790.00 Matches: 339			
Percent Similarity: 100.00% Conservative: 0			
Best Local Similarity: 100.00% Mismatches: 0			
Query Match: 100.00% Indels: 0			
DB: 3 Gaps: 0			
US-10-750-262-2 (1-339) x US-09-780-669-878 (1-1195)			
Qy	1	MecGluSerArgIysAspIleThrAsnGlnGluIleuTrpIysMetIysProArgArg	20
Db	66	ATGGAAGAGCAAGAAAGACATCAACCAAGAAAGAACTTTGGAAAAATGAAGCCTAGAGAG	125
Qy	21	AsnIeuGlnIuAspAspTyrIleuHISlysAspThrGlyIuThrSerMetIeIysArg	40
Db	126	AAATTGAAAGAAAGACGATTATTGGCATTAAGGACACCGGAGAGACCGATGCTTAAAAAGA	185
Qy	41	ProValIeuIeuHISleuHISGlnThrAlaHISAlaAspGluPheAspCysProSerGlu	60
Db	186	CTGTGTGTTTTGCAATTGACCAACCAAGCCCATGTGATGAATTTGACTGCCCTCAGAA	245
Qy	61	LeuGlnHISThrGlnIuIeuPheProGlnTrpHISleuProIleIysIleAlaIle	80
Db	246	CTTCACACACACAGAACTCTTTCCACAGTGGCACTTCCCAATTAATTAAGCTGCTATT	305

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QY      81  IleaaserleuthrphleuTyrrhrleuenuarvgiua11lehaProleu1aThr 100
      |||
Db      306  ATAGCATCTCGACTTCTTCTTACACTCTTCGAGGGAAGTAATTCACCCCTTTAGCAACT 365
QY      101  SerHsgInGIntYrPheTyRysIleProIleuVal11leasnlyeValleuProMet 120
      |||
Db      366  TCCCATCAACATATTTTATTAATTCCAATCCCGCATCAACAAAGCTTGGCAATG 425
QY      121  ValSerIlethrleu1aleuVal1yrieuProGlyVal11lealalaleValGln 140
      |||
Db      426  GTTTCATCACACTCTCTGGCATTTGGTTTACCTGCAGGCTGATGACGCAATTTGTCCA 485
QY      141  LeuH1saasnGlyThrylyTyRysPheProH1stRpleuAspLyseTrpMetleuThr 160
      |||
Db      486  CTTCAATATGGAACCAAGATAGAAGTTTCCACATGTTGATGATAGTGATGTTAA 545
QY      161  ArglyeGlnPhG1yleu1euserPhePhePha1aValleuH1sa1leTyRserleu 180
      |||
Db      546  AGAAAGCAGTTGGGCTTCTCAGTTCTTTTTCGTGACTGCATGCAATTTATAGTCTG 605
QY      181  SerTyRProMetArghrSerTyRarGlyTyRysleu1euanstTpa1aTyRgInGInVal 200
      |||
Db      606  TCTTACCAATAGAGCGGATCTTACAGATCAAGTTGCTAACTGGGCAATATCAACAGGTC 665
QY      201  GInGInasnlyeGluAspAlaTrp11leGlnH1saAspVal1TrpArgMetGln1eTyRVal 220
      |||
Db      666  CAACAAATATGAAGAAATGCTGGATTTGAGCATGATGTTGGAAATGAGATTTATGTG 725
QY      221  SerH1sgInGIntYrPheTyRysIleProIleuVal11leasnlyeValleuProMet 240
      |||
Db      726  TCTCTGGAATTTGGGATTTGGCAATACGCTCTGTGGCTGTGACATTAATTCATCT 785
QY      241  ValSerAspSerleuthrTrpArgIupheH1stYr11leGlnSerlyleuGly11leVal 260
      |||
Db      786  GTGAGAGACTCTTGAACATGAGAGAAATTCACATATTTCAAGAGCAAGTGAATTTGTT 845
QY      261  Serleu1euleuGlyThr11leH1sa1leu11lePhe1a1TrpAsnlyeSTrp1leAsp1le 280
      |||
Db      846  TCCCTTCTACTGGGCAATACACGCAATGATTTTTCCTGGAATGATGATGATATA 905
QY      281  LysGlnPheVal1TrpTyRTrpProThrPheMet11lealalalePheleuProIleVal 300
      |||
Db      906  AAACAAATTTGATGATATACCTCCCAACTTTATGATAGTCTGTTTCTTCCAAATGTT 965
QY      301  Valleu1lePhe1ySer11leuPhe1euproCysleuArglye1y11leu1y11le 320
      |||
Db      966  GTCTGATATTTAAAGCATATCTATCTCGCATGCTTGAAGAAAGATATCTGAAGATT 1025
QY      321  ArgH1sgIyTrpGluAspVal1Thry11leasnlyeSThrGln1eCysSerGlnleu 339
      |||
Db      1026  AGACATGTTGGGAAGACGTCAACCAAAATTAACAAACTGAGATATGTTCCAGTTG 1082

RESULT 12
US-09-822-827-878
; Sequence 878, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-878
Alignment Scores:

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Pred. No.: 1,676-1,995 Length: 1,195
Score: 1790.00 Matches: 339
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-750-262-2 (1-339) x US-09-822-827-878 (1-1195)

QY      1  MetG1userArglysaAsp1leThrAsnGlnGlu1eUtrpLyseMetlyeProArgArg 20
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Db      66  ATGGAAGCAACAAAGACATCACAAACCAAGAAACCTTGGAAATGAAGCTTAGAGA 125
QY      21  AsnleuGluGluAspArpTyRleuH1slysaAspThrGlyGluThrSerMetleu1ySaRg 40
      |||
Db      126  AATTTAGAAGAAAGCATTTATTTGCATTAAGACACGGAGAGACACAGATCTTAAAAAGA 185
QY      41  ProValleuLeuH1sleuH1eg1nthra1aH1saAspGluPheAspCysProSerGlu 60
      |||
Db      186  CCTGTGCTTTTGCAATTTGCACCAACAGCCCATGCTGATGATTAATTTGACTGCCCTTCA 245
QY      61  LeuGlnH1sthrGlnGlu1eupheProGlntrpH1sleuPro11elys11lealalale 80
      |||
Db      246  CTTCAACACACACAGAACTCTTCCACATGGCACTTGGCAATTTAAATAGCTGTATTT 305
QY      81  IleaaserleuthrphleuTyrrhrleuenuarvgiua11lehaProleu1aThr 100
      |||
Db      306  ATAGCATCTCGACTTCTTCTTACACTCTTCGAGGGAAGTAATTCACCCCTTTAGCAACT 365
QY      101  SerH1sgInGIntYrPheTyRysIleProIleuVal11leasnlyeValleuProMet 120
      |||
Db      366  TCCCATCAACATATTTTATTAATTCCAATCCCGCATCAACAAAGCTTGGCAATG 425
QY      121  ValSerIlethrleu1aleuVal1yrieuProGlyVal11lealalaleValGln 140
      |||
Db      426  GTTTCATCACACTCTCTGGCATTTGGTTTACCTGCAGGCTGATGACGCAATTTGTCCA 485
QY      141  LeuH1saasnGlyThrylyTyRysPheProH1stRpleuAspLyseTrpMetleuThr 160
      |||
Db      486  CTTCAATATGGAACCAAGATAGAAGTTTCCACATGTTGATGATAGTGATGTTAA 545
QY      161  ArglyeGlnPhG1yleu1euserPhePhePha1aValleuH1sa1leTyRserleu 180
      |||
Db      546  AGAAAGCAGTTGGGCTTCTCAGTTCTTTTTCGTGACTGCATGCAATTTATAGTCTG 605
QY      181  SerTyRProMetArghrSerTyRarGlyTyRysleu1euanstTpa1aTyRgInGInVal 200
      |||
Db      606  TCTTACCAATAGAGCGGATCTTACAGATCAAGTTGCTAACTGGGCAATATCAACAGGTC 665
QY      201  GInGInasnlyeGluAspAlaTrp11leGlnH1saAspVal1TrpArgMetGln1eTyRVal 220
      |||
Db      666  CAACAAATATGAAGAAATGCTGGATTTGAGCATGATGTTGGAAATGAGATTTATGTG 725
QY      221  SerleuGly11leValGlyleu1aleu1aleu1aleu1aleu1aleu1aleu1aleu 240
      |||
Db      726  TCTCTGGAATTTGGGATTTGGCAATACGCTCTGTGGCTGTGACATTAATTCATCT 785
QY      241  ValSerAspSerleuthrTrpArgIupheH1stYr11leGlnSerlyleuGly11leVal 260
      |||
Db      786  GTGAGTACCTCTTGAACATGAGAGAAATTCACATATTTCAAGAGCAAGTGAATTTGTT 845
QY      261  Serleu1euleuGlyThr11leH1sa1leu11lePhe1a1TrpAsnlyeSTrp1leAsp1le 280
      |||
Db      846  TCCCTTCTACTGGGCAATACACGCAATGATTTTTCCTGGAATGATGATGATATA 905
QY      281  LysGlnPheVal1TrpTyRTrpProThrPheMet11lealalalePheleuProIleVal 300
      |||
Db      906  AAACAAATTTGATGATATACCTCCCAACTTTATGATAGTCTGTTTCTTCCAAATGTT 965
QY      301  Valleu1lePhe1ySer11leuPhe1euproCysleuArglye1y11leu1y11le 320
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Db      966  GTCTGATATTTAAAGCATATCTATCTCGCATGCTTGAAGAAAGATATCTGAAGATT 1025

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QY 321 ArgHISGLYTRPGIUAAPVALThrlYsIleAsnLYsThrGluTlleCYsSerGlnLeu 339
 Db 1026 AGACATGGTTGGAGAGCGTACCAAAATTAACTAGATATGTTCCAGTTG 1082
 RESULT 13:00
 US-09-895-793-878
 / Sequence 878, Application US/09895793
 / Publication No. US20020192763A1
 / GENERAL INFORMATION:
 / APPLICANT: Xu, Jiangchun
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: Harlocker, Susan L.
 / APPLICANT: Jiang, Yuguu
 / APPLICANT: Kalos, Michael D.
 / APPLICANT: Retter, Marc W.
 / APPLICANT: Stolk, John A.
 / APPLICANT: Day, Craig H.
 / APPLICANT: Vedvick, Thomas S.
 / APPLICANT: Carter, Darrick
 / APPLICANT: Li, Samuel X.
 / APPLICANT: Wang, Aljun
 / APPLICANT: Skeiky, Yasir A.W.
 / APPLICANT: Heppler, William T.
 / APPLICANT: Henderson, Robert A.
 / APPLICANT: Hural, John
 / APPLICANT: McNeill, Patricia D.
 / APPLICANT: Houghton, Raymond L.
 / APPLICANT: Vinals de Basols, Carleota
 / APPLICANT: Foy, Teresa
 / APPLICANT: Fanger, Gary R.
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 / TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 / FILE REFERENCE: 210121.534C2
 / CURRENT APPLICATION NUMBER: US/09/895,793
 / NUMBER OF SEQ ID NOS: 982
 / SOFTWARE: FastSeq for Windows Version 3.0
 / SEQ ID NO 878
 / LENGTH: 1195
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / US-09-895-793-878
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 Score: 1790.00 Matches: 339
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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 QY 41 ProValLeuLeuHISLeuHISGlnThrAlaHISAlaAspGluLeuAspCysProSerGlu 60
 Db 186 CCGTGCTTTTGCATTTGACCAACCAAGCCCATGCTGATGAATTTTACCTGCCCTTCAGAA 245
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 QY 101 SerHISGlnGlnTrpPheTrpLYsIleProIleLeuValIleAsnLYsValLeuProMet 120
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 QY 121 ValSerIleThrLeuLeuAlaLeuValLYsLeuProGlnValIleAlaIleValGln 140
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 / Sequence 878, Application US/09895814
 / Publication No. US20020193296A1
 / GENERAL INFORMATION:
 / APPLICANT: Xu, Jiangchun
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: Harlocker, Susan L.
 / APPLICANT: Jiang, Yuguu
 / APPLICANT: Kalos, Michael D.
 / APPLICANT: Retter, Marc W.
 / APPLICANT: Stolk, John A.
 / APPLICANT: Day, Craig H.
 / APPLICANT: Vedvick, Thomas S.
 / APPLICANT: Carter, Darrick
 / APPLICANT: Li, Samuel X.
 / APPLICANT: Wang, Aljun
 / APPLICANT: Skeiky, Yasir A.W.
 / APPLICANT: Heppler, William T.
 / APPLICANT: Henderson, Robert A.
 / APPLICANT: Hural, John
 / APPLICANT: McNeill, Patricia D.
 / APPLICANT: Houghton, Raymond L.

```

; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-895-814-878

Alignment Scores:
Pred. No.: 1,67e-195 Length: 1195
Score: 1790.00 Matches: 339
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-750-262-2 (1-339) x US-09-895-814-878 (1-1195)

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QY 21 AsnLeuGlnGluAspArgTrpLeuHisLysAspThrGlyLysSerMetLeuLysArg 40
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QY 141 LeuHisAsnGlnTrpTrpLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
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Db 606 TCTTACCAATGAGGCGATCTCAAGATACAAAGTTGCTAACTGGGCAATATCAACAGGTC 665
QY 201 GlnGlnAsnLysGluAspAlaTrpLysIleAspValITPArgMetGluIleTrpVal 220
Db 666 CAACAAATTAAGAAAGATGCTGAGTGAATGATGTTTGGAGAAATGAGATTTATGTG 725
QY 221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValTrpSerIleProSer 240
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; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuguu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Mantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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; CURRENT FILING DATE: 2001-12-10
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; SEQ ID NO 878
; LENGTH: 1195
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; ORGANISM: Homo sapiens
; US-10-012-896-878

Alignment Scores:
Pred. No.: 1,67e-195 Length: 1195
Score: 1790.00 Matches: 339
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-750-262-2 (1-339) x US-10-012-896-878 (1-1195)
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QY 1 MetGluSerArgLysAspIleThrAsnGlnGluLeuTyrPheLysProArgArg 20
 Db 66 ATGGAAAGCGAAGAAAGCATACAAACAAAGAACTTTGGAAATGAAGCTTAGAGA 125
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 Job time : 959 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 6, 2005, 16:29:58 / Search time 159 Seconds

(Without alignments)
663.545 Million cell updates/sec

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Perfect score: 1790

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	90.5	5.1	1564	7	US-11-110-977-1
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11	87	4.9	3301	6	US-10-793-626-4209	Sequence 4209, Ap
12	87	4.9	4071	6	US-10-793-626-3381	Sequence 3381, Ap
13	86	4.8	1068	6	US-10-467-657-4965	Sequence 4965, Ap
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17	85	4.7	1368	7	US-11-074-176-237	Sequence 237, App
18	85	4.7	1517	6	US-10-750-185-26344	Sequence 26344, A
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42	80	4.5	1347	6	US-10-467-657-677	Sequence 677, App
43	80	4.5	3976	6	US-10-750-185-60435	Sequence 60435, A
44	80	4.5	5099	6	US-10-821-234-193	Sequence 193, App
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ALIGNMENTS

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; Sequence 3842, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUB480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3842
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3842

Alignment Scores:

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Score:	107.00	Matches:	64
Percent Similarity:	44.07%	Conservative:	55
Best Local Similarity:	23.70%	Mismatches:	94
Query Match:	5.98%	Indels:	58
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US-10-750-262-2 (1-339) x US-10-793-626-3842 (1-3137)

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US-10-750-185-29256
; Sequence 29256, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29256
; LENGTH: 2803
; ORGANISM: Bovine 1986680686697
US-10-750-185-29256

Alignment Scores:
Pred. No.: 1 13
Score: 99.50 Length: 2803
Percent Similarity: 34.15% Matches: 75
Best Local Similarity: 20.33% Mismatches: 51
Query Match: 5.56% Indels: 100
Gaps: 143
DB: 6 Gaps: 18

US-10-750-262-2 (1-339) x US-10-750-185-29256 (1-2803)
Qy      17 LysProArgArgAsnLeuGluIleuPheLeuPheLeuPheLeuPheLeuPheLeuPheLeu 30
Db      1251 AGGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1307
Qy      31 AspThrGlyGluThrSerMetLeuLeuArgProValLeuLeuIleuIleuIleuIleuIleuIleu 50
Db      1308 -----GGGAGGTATTTCAGAGCTG----- 1325
Qy      51 HisAlaAspGluPheAspCysProSerGluLeu----- 61
Db      1326 -----TCTTCACCTCCTTGTGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1367
Qy      62 GlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleuIleuIleuIleuIleuIleuIleu 81
Db      1368 GACCAACACACAA-----ACTTGACCTTTGAA----- 1394
Qy      82 AlaSerLeuThrPheLeuThrLeuLeuArgGluValIleHisProLeuAlaThrSer 101
Db      1395 -----ACAAATGTGAAAAAATAATATGAGCACTACCCAC-----ACCAAA 1436
Qy      102 HisGlnGlnTrpPheThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 121
Db      1437 CATCACTCACTGTTTAT-----CTTTTA 1460
Qy      122 SerIleThrLeuLeuAlaLeuValIleuProGluValIleAlaIleIleValGlnLeu 141

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Db      1461 TTTCGAACCTTTGTGCAGAAACCTTCTGACGAAATTCATGCTGACAGAAATATATTAA 1520
Qy      142 HisAsnGlyThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 161
Db      1521 TGTCTGTTCCGAG-----GATGTGTGATGCTTACTGATGTCACAA 1565
Qy      162 LysGln-----PheGlyLeuLeu 167
Db      1566 AAAAGAAATGGAACGGGGCAAAAAGAAAGATGACGAGTATTATTATCATTAACCTTCC 1625
Qy      168 SerPhePhePheAlaValLeuHis-----AlaIleuIleu 178
Db      1626 CTCTTCTTGTCCCTGATCTCATGCTTAAATCTCTGACAAATGCTGCTGCTACCG 1685
Qy      179 SerLeuSerIleuProMetArgArgSerIleuIleuIleuIleuIleuIleuIleuIleuIleu 191
Db      1686 TCTGTCACACATTAATTAAGAAAGTACTACGACCAAGATTAACAGCCATCATTAAGA 1745
Qy      192 -----LeuLeuAsnTrpAlaIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 209
Db      1746 GAGAGATTAAGAAATTTGTTCTTACTCTGTTCTGACAGACAGACAGATTAAGAA 1805
Qy      210 GlnHisAspValTrpArg-----MetGluIle 218
Db      1806 CAACGAGCTTGTCTGCGCCCAACAAACAGAGCCGTGTAAGTATGATGAGAGAGT 1865
Qy      219 TyrValSerLeuGlyIleValIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleu 238
Db      1866 TACTTTCACTGCTGCGCTGACAGAGGTTTCCGTGTGCT--CAGCGGTAAAGAAATCTG 1922
Qy      239 ProSerValSerAsp-----SerLeuThrTrpArgGluPheIleuIleuIleuIleuIleuIleu 254
Db      1923 CTTCACTGACGAGAGACAGAGGCTCACTCCCTGCGCTGGAGAAC-----CCTCTGGAG 1976
Qy      255 SerIleuLeuGlyIleValSerLeuLeu----- 264
Db      1977 AAGAAATGGAACTACTCAGATTTCTTGAAGTGAAGAGTTCGTCGAGTAACGCC 2036
Qy      265 -----GlyThrIleHisAlaLeuIlePheAlaTrpAsnIleTrpIleAspIleuIleuIleuIleu 282
Db      2037 TGAAGGCTCACTGTCACAGGGGTTCCAAAGATGATGAAGATGCGACACTACTGAG 2096
Qy      283 PheValTrpThrProThrProThrPheMetIleAlaValPheLeuProIleValIleu 302
Db      2097 -----CGACTAACCTTTCACCTTGTGCTTGG 2123

RESULT 4
US-10-793-626-1307
; Sequence 1307, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUI480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1307
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-1307

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Oy      173 ValLeuHnSaIaIeYrSerLeuSeTyPro-----MetArgRgSer 187
Db      856 ATAAAGATGATAAATTCTTAACCTTATTATTACAGGAACAGATTATTATTGTGGCTTA 915
Oy      188 TYArGrTYrLYsLeuLeuAsnTPtAlaTyrcInGIlnValGInGIlnAsnLYsGLubSpAla 207
Db      916 TTTATGTCGAATTAAATGACAGTGAGTACAATCCACGTAATTCAAGCGTATTATTGAA 975
Oy      208 TPrlleGIlnHisAspVal-----TPArMgcGuileTYrValSerLeu 222
Db      976 CACGTGCAGAGATACACAGCAGCATGATGATGGATTGCTG-----AGCTTC 1026
Oy      223 -----GlyILEvalGlyLeuAlalleuAlaleuAlaLeuAlaVal 235
Db      1027 AATGCCGATTTGCGCGTGGCCGATGCGTAGTGAACCTGTTATGACACTTATTCAGTcG 1086
Oy      236 ThrSerlleProSerValSerAspSerLeuThrTPArGslubHehISYrllleGlnSer 255
Db      1087 GAATATGTTACT-----TATACTAGTGA 1110
Oy      256 lYsLeuGlYrLEvalSerLeuLeu 264
Db      1111 TTGATAGGTTTAAATTAAGTCTTATCATT 1137

RESULT 7
US-11-110-977-1
; Sequence 1, Application US/11110977
; Publication No. US20050260682A1
GENERAL INFORMATION:
; APPLICANT: Charney, Patrick R.
; APPLICANT: Smith, Ryan C.
; APPLICANT: Argonza-Barrett, Rhodora H.
; APPLICANT: Fitzgibbon, Matthew P.
; APPLICANT: Wang, Kai P.
TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
FILE REFERENCE: CECH118764
CURRENT APPLICATION NUMBER: US/11/110,977
PRIOR FILING DATE: 2005-04-19
PRIOR APPLICATION NUMBER: US/10/112,645
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/280,514
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1564
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (314)..(1138)
OTHER INFORMATION:
US-11-110-977-1

Alignment Scores:
Pred. No.:          5.26           Length:         1564
Score:              90.50           Matches:        42
Percent Similarity: 39.91%           Conservative:   49
Best Local Similarity: 18.42%       Mismatches:    75
Query Match:        5.05$            Gaps:          62
DB:                  7               Indels:         8

US-10-750-262-2 (1-339) x US-11-110-977-1 (1-1564)
Oy      134 ValILleAlaLaIeValGInLeuHIsAnGlyThryLySTyrLYsLYsrhePrOHISTrP 153
Db      286 GTGTGTAGTAAACAGACCAAAGTTGGATCATGGGGAATTTCAAGKGTATCCSCCTCG 345
Oy      154 LeuAspLYrTPmTeLcuThrArGlyvGInPhGeGlyLeuLeuSerPerhePeAlaVal 173
Db      346 -----AACCTTCTTTTATTATTAGTGTCTTG 372

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QY	19	ATGATGAsnLeuGlnGlnuAAspArgTrpLeuHisGlyAspThrGlnGlyThrSerMetLeu	38
Db	252	CGGCAAAACCTTTTTCAGACGGC-----	275
QY	39	LyAspArgProValLeuLeuHis-----LeuHisGlnProAlaHisAlaAspGlnPheAsp	56
Db	276	AATCAACCCCTGCTTTGTGTGATCCCGCATTTGTCTACGCTTTTCACTGGATCAAGCTTAC	335
QY	57	CysProSerGlnLeu-----GlnHisThrGlnGlnLeu-PheProGln	70
Db	336	CTTCCGGCTGGAAAGATTTTGGGGGACAGTGAATGATTATAGACCTGTGCTCGTTCCGCT	395
QY	70	nThrPheLeuProGlnLeuGlyLeuAlaAlaIleIleAlaSerLeuThrPheLeuTyThyle	90
Db	396	CGGCTACCTGCGGCTGGAGGGGCGCATCAACCGCATACCGCTGTCTTAC-----	444
QY	90	uLeuArgGlnValIleHisProGlnAlaThrSerHisGlnGlnTyPheTyPheGlyAlaPhe	110
Db	445	---GAAGAAGTCAGCGCTGCTTGGGCAAAAGCGCGCTGCAAACCTTTTTC-----	495
QY	110	oIleLeuValIleAsnLysValLeuProMetVal-----SerIleThrLeuAlaIle	128
Db	496	---GCCATCTCCCAACAGCTCAAAACCGGCATCGGACAGAGGCTGTACTGATCGCGCT	551
QY	128	uValTyPheLeu-----ProGlnValIleAlaAla	137
Db	552	GCATATGCTGTGCGAATTGGACGGCGATCATTTTGAATCAACCCCACTTTTACACATCG	611
QY	137	AlIleValGlnLeuHisAsnGlnTyHisTyPheProHisTyPheAspLysTrp	157
Db	612	CATTTTCCAAATAATACGA--ATGCTCTACAAACATACATCCGCGCGCTTTCGCC	668
QY	157	pMetLeuThrArgLysGlnPheGlyLeuLeuSerPhePheAlaValLeuHisAla--	176
Db	669	TGTTTGTGACG--GCGGTGCGCGCATCGTCGTATTTGGAAAGAAGCATATTGCGGCGCA	725
QY	177	---IleTySerLeuSerTyPheMetArgArgSerTyArgTyPheLeuLeu	194
Db	726	ACCCAAAGATTTTACACAGCGCAAGGGGTGCGCGTCTTATCCCGTCAAAACCTTC--	783
QY	194	nThrAlaTyGlnGlnValGlnGlnAsnLysGlnAspAlaTrpIleGlnHisAspValTr	214
Db	784	---AAACCTCCCGTCAGATCGGCGCGATGTTT	815
QY	214	pArgMetGlnLeuTyPheValSerLeuGlyIleVal-----GlyLeuAlaIleLeuAl	231
Db	816	TTTAAAGCAGCTTGATGATT--TTGGCATATATATCCCTTGGCGATGATGATCAATGG	872
QY	231	AlaLeuAlaValAlaThrSer-----IleProSerValSerAspSerLeuThrTr	247
Db	873	GATGATGCGTGGCAGCTTCCGGCAGATCCGCGCTCGTATCCGATTTGTATGCC-----	924
QY	247	pArgGlnPheHisTyPheGlnSer--LysLeuGlyIleValSerLeuLeuLeuGlyTh	266
Db	925	---TTATCCGTTCTTAAGCGTATCGGCTTATCGGCTTATAGGTGGCATTTTGACAT	971
QY	266	rIleHisAlaLeuIlePheAlaTrp-----AsnLysTrp	277
Db	972	ATTATGCTGCTTGGCCCTTGTGGGACATCGGTTGCGATATGCAATTTTAAACCGTTTG	1031
QY	277	pIleAspIleLysGlnPheValTrpTyThrProThrPheMetIleAlaValPheLe	297
Db	1032	GATAGACAGGCTGCGTTTACTGCACGCGCTCCCGGTTTGGTTATCGGCTTATCCTT	1091
QY	297	uPro-----IleAlaValLeuIle	303
Db	1092	GGTTATTTACAGATCAATACACCCCTGCGTTTACCAAACTTTATCGTGTATCTCT	1155
QY	303	ePheLysSerIleLeuPheLeuPro-----CysLeuArgLysLysIleLeuLys	319
Db	1152	TGCGTATTCATGCTTACTCTGCCAGTATGCCGAATACCAACCAACCTTGAAGATCTCTTGAAACA	1211

Oy	149	-----LysPheProHisIleTrpLeuAspArgIleTyrMet-----LeuThr-----Argly	162
Db	184235	TTTTATATCATCTCTCATTGAGCTTTAGAAATTTGGTTTCACGGCTTAACGTAAATGAAGAAG	184295
Oy	162	s-----GlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerIle	180
Db	184295	GATTTAAAATTCTCTCTCTCTCTCTCTCTGCATTGCTAAGCCCTTGACCATTCCATATGTCT	18435-
Oy	180	user-----TyrPrometArGserTyrArgTylrYlsIeule	193
Db	184355	TACTGTGGCTGTGACCTCTCGTTTCCAGTC-----TATAATCTCTG	184395
Oy	193	wAnETPrLaITyrglGlnIValGlndIAsnlysvGIuAspAlaTPrlEGlnHIsArVa	213
Db	184400	CtAtAgGGgATATCAAAAACTTAGTC--AcTAAATCAAAGAGAGCTGTGCCAGATGT	184457
Oy	213	1-----Trp-----ArgmetGluIleTyrValSerIe	222
Db	184458	GACTGTGAGATTATAGCTGTCTGTGGCTTGTGGCTCCCCAAAGAACAGCTATGCAAGCCG	184517
Oy	222	ugIlyIleValIGlyLeuAlaIleLeuAlaLeuAlaValThnSerIleProSerValse	242
Db	184518	TGGCTCCAGAAAAGGAGAGGTGTtAGTCAGTTGT-----TCGGCTTC	184559
Oy	242	rAerSerLeuThITrPAvg-----	248
Db	184560	CTCTGTGTCTTACCTTCAGGTTTAAATCAAGTAAGCTTGGCAGTATTTACTCCCTGTGG	184619
Oy	249	-----GluPheIleTyrIleGlnSerYlsleuGlyIleValSerIeule	264
Db	184620	GACACATGTCGATCAGTACCTTGTGCAGATACAAAGATGTGGCTGTCT---CTCATTTCT	184676
Oy	264	uGIyThrlenIleAlaLeuIlePheAlaTrpAsnlyStrIleAspIleIelYglInPheVa	284
Db	184677	AACAACCATC-----	184686
Oy	284	lTPryThrProPOThrPheMetIlAlaValPheLeuproIleValIleuIleph	304
Db	184687	-TGGTGcAGTgTACCTCACTTGTGTATAGATTATTTCTGTAGTttTATCTGTtt	184745
Oy	304 e 304		
Db	184746	T 184746	

RESULT 10
US-10-793-626-4225/c
; Sequence 4225, Application US/10793626
; Publication No. US20050255478A1
GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4225
LENGTH: 3083
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-4225

Alignment Scores:	37.9	length:	3083
Pred. No.:	87.00	Matches:	80
Percent Similarity:	32.58%	Conservative:	35
Best Local Similarity:	22.66%	Mismatches:	103
Query Match:	4.86%	Indels:	135

Db 2031 TGAATTCGCTGATATCGCGTTTGCATTAATTCGATTCGCGCATTAAGCGGT 1972
 Qy 236 rSerileProSerValSerApeSerLeuThrTTPArgGluPheHisTyrIleGlnSerly 256
 Db 1971 TACATTAACCAAAAGTTGCG-----ATACATTTGGGTGATAGA 1933
 Qy 256 sLeuGly-----IleValSerLeuLeuGlyThrIleHisAlaLeu----- 271
 Db 1932 CTAGGCGCAATTAATTTATTTATTTCTTGGTGAAGATAGTGTCATCTTGATGACATT 1873
 Qy 272 -----Ph 272
 Db 1872 TGCAGCACTGTTGTTGTAGAAATTTGATAAATATCCAGACTGAAGTGTGCGTT 1813
 Qy 272 eAlaTTPAsnlySTripIleAspIleGlnPheVal-TTPYrThrProProThrPheM 292
 Db 1812 TGCATTTGAGTGTGGGTAGGTATTAACCTGTTAATAATGTAC----- 1769
 Qy 292 eCilleAlaValPheLeuProIleValIleuIlePhe 304
 Db 1768 -----TTGCACATCTGATATTTGCGGTTT 1745

RESULT 12
 US-10-793-626-3381/c
 ; Sequence 3381, Application US/10793626
 ; Publication No. US2005025478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PUS48005
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; CURRENT FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 3381
 ; LENGTH: 4071
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: nucleic acid sequence
 US-10-793-626-3381

Alignment Scores:
 Pred. No.: 57.9 Length: 4071
 Score: 87.00 Matches: 67
 Percent Similarity: 35.71% Conservative: 38
 Best Local Similarity: 22.79% Mismatches: 95
 Query Match: 4.86% Indels: 94
 Gaps: 13

US-10-750-262-2 (1-339) x US-10-793-626-3381 (1-4071)
 Qy 73 LeuProIleuValIleAlaIleIleAlaSerLeuThrPheLeuTyrThrLeuLeu-Ar 92
 Db 1305 CTTCGCGTAAAGTGGGCAAAAATATTTCTAAGTAGACCTTTGCTATTAATAGCATAG 1246
 Qy 92 gCilaValIleHisProLeuAlaThrSerHisGlnGlnIleTyrPheTyr-----Ly 108
 Db 1245 GTCTCTT-----TATTTGATTTAAACTAAAGGA 1216
 Qy 108 eIleProIleLeuValIleAlaValIleuProMetValSerIleThrLeuLeuAlaLe 128
 Db 1215 GTTGTCCACAAATGATCCGAGTTTGATTTTACCTTATTTATGGGTA---CTTTAGTACT 1159
 Qy 128 uValIleuProGlyValIleAlaIleValIleGlnLeuHisAsnGlyThrIleTyrIly 148
 Db 1158 TGAATTTTGAAGAATATTTAGCACTGATTAATGCAATTTGTAATGCGGTAATGCTTAA 1099
 Qy 148 slyPheProHisSTripLeuAspIleTyrMetLeuThrArgIleGlnPheGlyLeuLeu 168

Db 1098 ACACTTACCACTTAACCAACGTAATAAAGACACTTTT-----TATGCGCTATTAGG 1048
 Qy 168 rPhePhePheAlaValLeuHisAlaIleTyrSerLeuSer----- 181
 Db 1047 TGCATTCATTTTATAGTATTTATGCTTATTTTAAATAGTATTTATTCGAACTTGTGTC 988
 Qy 182 -----TyrProMetArgArgSerTyrArgTyrIleLeuLeu 194
 Db 987 GATTCAAGCAGCAGGTCTGTTTACTTATCTATATGTCTATTAA---AATTTATGGA 931
 Qy 194 nTTPAlaTyrGlnGlnValGlnGlnAsnlySgluAspAlaTTPIleGluHis----- 211
 Db 930 ATTTTTCATCATGTCATTAATGAATAAACACCATTAAGAACAGAGACGAAATCATTTGCA 871
 Qy 212 -----AspValITTPArgMetGluIleTyrVa 220
 Db 870 TGAACAGGCAACGAAAAAGAGTAGCCCTTAATCTTTTGGGGAACGATTTTAAAGT 811
 Qy 220 lSerLeuGlyIleValIleGlyLeuAlaIle-----LeuAlaLeuAlaVal---Th 236
 Db 810 TGAATTCGCTGATTCGCGGTTTGCATTTGATTCGATTCGCGCATTTAGCCATGACCGT 751
 Qy 236 rSerileProSerValSerApeSerLeuThrTTPArgGluPheHisTyrIleGlnSerly 256
 Db 750 TACATTAACCAAAAGTTGCG-----ATACATTTGGGTGATAGA 712
 Qy 256 sLeuGly-----IleValSerLeuLeuGlyThrIleHisAlaLeu----- 271
 Db 711 CTAGGCGCAATTAATTTATTTATTTCTTGGTGAAGATAGTGTCATCTTGATGACATT 652
 Qy 272 -----Ph 272
 Db 651 TGCAGCACTGTTGTTGTAGAAATTTGATAAATATCCAGACTGAAGTGTGCGTT 592
 Qy 272 eAlaTTPAsnlySTripIleAspIleGlnPheVal-TTPYrThrProProThrPheM 292
 Db 591 TGCATTTGAGTGTGGGTAGGTATTAACCTGTTAATAATGTAC----- 548
 Qy 292 eCilleAlaValPheLeuProIleValIleuIlePhe 304
 Db 547 -----TTGCACATCTGATATTTGCGGTTT 524

RESULT 13
 US-10-467-657-4965
 ; Sequence 4965, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 4965
 ; LENGTH: 1068
 ; TYPE: DNA
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-4965
 Alignment Scores:
 Pred. No.: 9.9 Length: 1068
 Score: 86.00 Matches: 67
 Percent Similarity: 37.09% Conservative: 45
 Best Local Similarity: 22.19% Mismatches: 112
 Query Match: 4.80% Indels: 78

Oy		105	TyPheTyTysIlePro-IleLeuValIleAsnLysValLeuProMetValSerIleTh	124
			::: ::: ::: :::	
Dd		1426	TATGGTAGCTAGTGCCCACTATTATGCCATTGATAAACAAGTTTGTACTATT	1367
Oy		124	rLeuLeuAlaLeuValTyLeuProGlyValIleAlaIleValGlnLeuHisAsnGl	144
			::: ::: ::: ::: :::	
Dd		1366	TTGGATTATTCCTCATTACCTAGCTACTGGTTGGCCACTGCTGAAGTGGTTTTCTACTT	1307
Oy		144	yThrLyTyTLyAlaLysPheProHIStrPLeuAspLysTrpMetLeuthrArgLysGln--	163
			::: ::: ::: :::	
Dd		1306	CTTTAAAGTAGCAACTTCTCCACCCTCGCTTCACTTGGCTGGCGAGGCAGATTCCGAG	1247

Search completed: December 6, 2005, 18:50:55
Job time : 320 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 6, 2005, 16:29:53 (Search time 200 Seconds
(without alignments)
3012.967 Million cell updates/sec

Title: US-10-750-262-2

Perfect score: 1790
Sequence: 1 MESRRDINQELMKKPRR.....IRHGWEDYTKINKTICGQL 339

Scoring table:

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Xgapop 10.0	Xgapext 0.5		
Ygapop 10.0	Ygapext 0.5		
Fgapop 6.0	Fgapext 7.0		
Delop 6.0	Delext 7.0		

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPFO.spool_h/US10750262/runat_06122005_162946_15642/app_query.fasta_1.519
-DB=Issued_Patents_NA -OPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MTN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US10750262 @CNC 1.1 193 @runat_06122005_162946_15642 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MAIN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/1.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP.COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE.COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1790	100.0	1193	3	US-09-455-486-1
2	1790	100.0	1195	3	US-09-323-873A-1
3	1790	100.0	1195	3	US-09-685-166A-878
4	1790	100.0	1195	3	US-09-679-426-878
5	1790	100.0	1195	3	US-09-759-143-878
6	1790	100.0	1195	3	US-10-010-667A-1
7	1790	100.0	1195	3	US-10-012-896-878
8	1790	99.6	1147	3	US-09-949-016-2686
9	1358.5	75.9	3627	3	US-09-323-873A-6

10	1358.5	75.9	3627	3	US-09-455-486-4	Sequence 4, Appl1
11	1358.5	75.9	3627	3	US-10-010-667A-6	Sequence 6, Appl1
12	1071.5	59.9	9073	3	US-09-949-016-14428	Sequence 14428, A
C 13	905	50.6	592	3	US-09-439-313-342	Sequence 342, App
C 14	905	50.6	592	3	US-09-352-616A-342	Sequence 342, App
C 15	905	50.6	592	3	US-09-636-215-342	Sequence 342, App
C 16	905	50.6	592	3	US-09-685-166A-342	Sequence 342, App
C 17	905	50.6	592	3	US-09-679-426-342	Sequence 342, App
C 18	905	50.6	592	3	US-09-759-143-342	Sequence 342, App
C 19	905	50.6	592	3	US-09-651-236-342	Sequence 342, App
C 20	905	50.6	592	3	US-09-657-279-342	Sequence 342, App
C 21	905	50.6	592	3	US-10-012-896-342	Sequence 342, App
C 22	741	41.4	2714	3	US-09-562-930-5	Sequence 5, Appl1
C 23	741	41.4	3884	3	US-09-562-930-10	Sequence 10, Appl1
C 24	717	40.1	2453	3	US-09-455-486-5	Sequence 5, Appl1
C 25	717	40.1	2469	3	US-10-104-047-1185	Sequence 1185, Ap
C 26	715	39.9	1403	3	US-10-104-047-1185	Sequence 1185, Ap
C 27	713.5	39.9	1886	3	US-10-012-896-995	Sequence 995, App
C 28	651	35.6	2118	3	US-09-562-930-1	Sequence 1, Appl1
C 29	637.5	35.6	2118	3	US-09-562-930-3	Sequence 3, Appl1
C 30	625	34.9	4429	3	US-09-455-486-7	Sequence 7, Appl1
C 31	607	33.9	848	3	US-10-012-896-993	Sequence 993, App
C 32	576	32.2	519	3	US-10-010-667A-7	Sequence 7, Appl1
C 33	576	32.2	521	3	US-09-323-873A-7	Sequence 7, Appl1
C 34	497	27.8	1213	3	US-09-083-521-3	Sequence 3, Appl1
C 35	450	25.1	455	3	US-09-621-976-9264	Sequence 9264, Ap
C 36	400	22.3	366	3	US-09-030-607-215	Sequence 215, App
C 37	400	22.3	366	3	US-09-439-313-215	Sequence 215, App
C 38	400	22.3	366	3	US-09-352-616A-215	Sequence 215, App
C 39	400	22.3	366	3	US-09-232-149A-215	Sequence 215, App
C 40	400	22.3	366	3	US-09-159-812-215	Sequence 215, App
C 41	400	22.3	366	3	US-09-636-215-215	Sequence 215, App
C 42	400	22.3	366	3	US-09-685-166A-215	Sequence 215, App
C 43	400	22.3	366	3	US-09-115-453-215	Sequence 215, App
C 44	400	22.3	366	3	US-09-688-489-215	Sequence 215, App
C 45	400	22.3	366	3	US-09-679-426-215	Sequence 215, App

ALIGNMENTS

RESULT 1
US-09-455-486-1
Sequence 1, Application US/09455486
Patent No. 6833438
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saitan
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
FILE REFERENCE: 129.17-US-11
CURRENT APPLICATION NUMBER: US/09/455,486
PRIORITY FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIORITY FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1193
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (64)...(1083)
US-09-455-486-1
Alignment Scores:
Pred. No.: 1 09e-202
Score: 1790.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Length: 1193
Matches: 339
Conservative: 0
Mismatch: 0

Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-750-262-2 (1-339) x US-09-455-486-1 (1-1193)

QY 1 MetGlusSerArglyAspIleThrAsnGlnGluLeuTyrPheMetLysProArgArg 20
DB 64 ATGGAACACAGAAAAGACATGACAAACCAAGAACTTTGGAAATGAAGCTTAGGAGA 123
QY 21 AsnLeuGlnGluAspArgTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
DB 124 AATTAGAAAGAGAGATTAATTTGATAGACAGAGGAGACAGACAGCATGCTTAAGAAAGA 183
QY 41 ProValLeuLeuHisLysGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
DB 184 CCTGGCTTTTGCATTTTGCACCAACAGCCCATGCTGATGATTTGACCTGCCCTCAGAA 243
QY 61 LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLysProIleLysIleAlaIle 80
DB 244 CTTTACACACACACAGAACTTTTCCACAGTGGACATTCCTCAATTAATTAAGCTGCTAAT 303
QY 81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
DB 304 ATAGCATCTCTGACCTTTTCTTACACTCTTGAGGGAAGTAATTCACCTTTAGCAACT 363
QY 101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
DB 364 TCCCATCAACAAATATTTATTAATAATTCATCTGCTGATCAACAAAGCTTTGCCAATG 423
QY 121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
DB 424 GTTTCCATCACTCTCTGGCATTTGGTTTACCTCCAGTGTGATAGACAGAAATTTGCCAA 483
QY 141 LeuHisAsnGlyThrLysTyrLysLysPheProHisIleTrpLeuAspLysIleTrpMetLeuThr 160
DB 484 CTTCAATTAAGGAACCAAGTATTAAGATTCCACATTTGTTGATGAAGTGAAGTTATACA 543
QY 161 ArgLysGlnPheGlyLeuLeuSerPhePheAlaValLeuHisAlaIleTyrSerLeu 180
DB 544 AGAAGACAGTTTGAGCTTCTCAAGTTCTTTTTCCTGCTACTGCATGCAATTTATAGCTG 603
QY 181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
DB 604 TCTTATCCCATGAGCGCATCTCAATACATCAAGTGTAAATCGGCATATCAACAGATC 663
QY 201 GlnGlnAsnLysGluAspAlaTyrPheIleGlnHisAspValTyrPheMetGluIleTyrVal 220
DB 664 CAACAAATTAAGAAAGATGCTGATTTGAGCATGATGTTTGGAATGGAATTTATGTG 723
QY 221 SerLeuGlyIleValIleGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
DB 724 TCTCTGGAAATTTGGGATTTGGCAATCTGACTCTGTTGGCTGTGACATCTATTCATCT 783
QY 241 ValSerAspSerLeuThrTyrPheGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
DB 784 GTGAGTACTCTTTGACATGAGAGAAATTTCACTATATTGACAGCAAGCTAGGAATTTGTT 843
QY 261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTyrPheAspLysTrpIleAspIle 280
DB 844 TCCCTTACTAGGACACATATACAGCATTTGATTTTGGCTGGAATTAAGTGAATGATATA 903
QY 281 LysGlnPheValTyrPyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
DB 904 AAACAAATTTGATGATATACCTTCAACTTTTATGATAGCTGTTTCTTCCAAATTTGTT 963
QY 301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysIleLeuLysIle 320
DB 964 GTTCTGATATTTAAAGACATACTATCTCGGCATCTTGAGGAGAAAGATCTGAAGATT 1023
QY 321 ArgHisGlyTyrPheGluAspValThrLysIleAsnLysTrpGlnIleCysSerGlnLeu 339
DB 1024 AGACATGTTGGGAGAGACGTCAACAAATTAACAAAACTGAGATATGTTCCAGTTG 1080

RESULT 2
US-09-323-873A-1
; Sequence 1, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USBS THEREOF
; FILE REFERENCE: 129.16USU2
; CURRENT APPLICATION NUMBER: US/09/323.873A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-323-873A-1

Alignment Scores:
Pred. No.: 1,09e-202 Length: 1195
Score: 1790.00 Matches: 339
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-750-262-2 (1-339) x US-09-323-873A-1 (1-1195)

QY 1 MetGlusSerArglyAspIleThrAsnGlnGluLeuTyrPheMetLysProArgArg 20
DB 66 ATGGAACACAGAAAAGACATGACAAACCAAGAACTTTGGAAATGAAGCTTAGGAGA 125
QY 21 AsnLeuGlnGluAspArgTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
DB 126 AATTAGAAAGAGAGATTAATTTGATAGACAGAGGAGACAGACATGCTTAAGAAAGA 185
QY 41 ProValLeuLeuHisLysGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
DB 186 CTTGCTTTTGCATTTTGCACCAACAGCCCATGCTGATGAATTTGACCTTCAGAA 245
QY 61 LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLysProIleLysIleAlaIle 80
DB 246 CTTACAGACACACAGAACTTTTCCACAGTGGCACTTGCATTAATAATTAAGCTGCTAAT 305
QY 81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
DB 306 ATAGCATCTCTGACTTTTCTTACACTCTTGAAGGAATTAATTCACCTTAGCAACT 365
QY 101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
DB 366 TCCCATCAACAAATATTTTAAATTTCAATCTGCTGATCAACAAAGCTTGGCAATG 425
QY 121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
DB 426 GTTTCCATCACTCTCTGGCATTTGGTTTACCTGCAAGTGTGATAGCAATTTGCTCAA 485
QY 141 LeuHisAsnGlyThrLysTyrLysLysPheProHisIleTrpLeuAspLysIleTrpMetLeuThr 160
DB 486 CTTCAATTAAGGAACCAAGTATTAAGATTCCACATTTGTTGATGAAGTGAATGTTAACA 545
QY 161 ArgLysGlnPheGlyLeuLeuSerPhePheAlaValLeuHisAlaIleTyrSerLeu 180
DB 546 AGAAGACAGTTTGAGCTTCTCAAGTTTCTTTTCTGCTGATGACATGAATTTATATAGCTG 605

[illegible]

Best Local Similarity: 100.00%

321 ArgHisGlyTrpGluAspValThrIleIleAsnLysThrGluIleCysSerGlnLeu 339
1026 AGACATGTTGGGAAGACGTCAACCAAAATTAACAAACTGAGATATGTTCCCACTTG 1082

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RESULT 4
US-09-679-426-878
; Sequence 878, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqun
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-679-426-878

Alignment Scores:
Pred. No.: 1.09e-202 Length: 1195
Score: 1790.00 Matches: 339
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-750-262-2 (1-339) x US-09-679-426-878 (1-1195)

QY 1 MetGluSerArgIysAspIleThrAsnGlnGluIleuTrpIysMetIysProIArg 20
DB 66 ATGGAAAGCGAAAGACATCAAAACCAAGAAAGAACTTTGGAAATGAAGCTTAGAGA 125
QY 21 AsnIleuGluIysAspIleThrAsnGlnGluIleuTrpIysMetIysProIArg 40
DB 126 AATTAGAAAGACATCAAAACCAAGAAAGAACTTTGGAAATGAAGCTTAGAGA 185
QY 41 ProValIleuLeuHisIleuHisGlnThrAlaHisAlaAspGluProIArg 60
DB 186 CCTGTGCTTTGGCAATTTGCAACCAAGCCATGCTGTAATTTGACTGCCCTTCAGAA 245
QY 61 LeuGlnHisThrGlnGluIleuPheProGlnTrpHisIleuProIleuVal 80
DB 246 CTTAGACACACAGAACTCTTTCCACAGTGGCACTTGCCAAATTAATAGCGCTATT 305
QY 81 IleAsnSerLeuThrPheLeuTrpIleuLeuArgIleuValIleHisProIleuAlaThr 100
DB 306 ATAGCATCTGACCTTTCTTTACACTCTTCTGAGGAGAAATTAATCACCCCTTAGCACT 365
QY 101 SerHisGlnGlnTrpPheTrpIysIleProIleuValIleAsnIleValIleuProIet 120
DB 366 TCCCATCAACATATATTTTAAATTCCAATCCGTGTCATCAACAAAGCTTGGCAATG 425
QY 121 ValSerIleThrLeuLeuAlaIleuValIleuProGlyValIleAlaAlaIleValGln 140
DB 426 GTTTCATCACTCTCTTGGCAATTTGTTTACTGCGCAGGTGATAGCGCAATTTGCCAA 485
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QY 141 LeuHisAsnGlnTrpIleuTrpIysIleuPheProHisTrpIleuAspIysTrpMetLeuThr 160
DB 486 CTTCATATATGAAACCAAGATTAAGAAATTTCCACATTTGGTGGATAGTGAATGTTTACA 545
QY 161 ArgIleuGlnPheGlyLeuLeuSerPhePheAlaValIleuHisAlaIleTrpSerLeu 180
DB 546 AGAAAGCAATTTGGGCTTCAAGTTCTTTTGGCTGATGCAATGCAATTTATAGCTG 605
QY 181 SerTrpProMetArgArgSerTrpArgTrpIysLeuLeuAsnTrpAlaTrpGlnGlnVal 200
DB 606 TCTTACCAATAGAGGCATCTCAAGATACAGATTAAGTTGTAACCTGGGATTAACAAGATC 665
QY 201 GlnGlnAsnIysGluIysAspIleuValIleGlnHisAspValTrpArgMetGluIleTrpVal 220
DB 666 CAACAAATTAAGAAATGCTGATTAAGCATGATGTTTGGAGAAATGGAATTTATGCTG 725
QY 221 SerIleuGlyIleValIleGlyLeuAlaIleuAlaIleuAlaIleuAlaIleuValTrpSerIleProSer 240
DB 726 TCTCTGGAAATTTGGGATTTGGCAATTCGCTGCTGGTGGCTGACATCTATTCACATCT 785
QY 241 ValSerAspSerLeuThrTrpArgGluPheHisTrpIleGlnSerIysLeuGlyIleVal 260
DB 786 GTGAGTACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTTAGAATGTT 845
QY 261 SerIleuLeuLeuGlyThrIleHisAlaIleuIlePheAlaTrpAsnIleTrpIleAspIle 280
DB 846 TCCCTTCACTGGGCAATACAGCATGATTTTGGCTGGATTAAGTGAATGATATATA 905
QY 281 IysGlnPheValIleTrpTrpThrProProThrPheMetIleAlaValPheLeuProIleVal 300
DB 906 AAACAAATTTGATGGATATACCTTCACTTTATAGTAGCTTTCTTCCAAATGTT 965
QY 301 ValIleuIlePheIysSerIleuPheLeuProCysLeuArgIysIleIleuIysIle 320
DB 966 GTCTGATATTTAAAGCACTATCTTCCGCACTTGAGGAAAGAACTAGTGAAGATT 1025
QY 321 ArgHisGlyTrpGluAspValIleTrpIleAsnIysThrGluIleCysSerGlnIleu 339
DB 1026 AGACATGCTTGGGAGAGACGTCAACAAATTAACAAACTGAGATATGTTCCAGATTG 1082

RESULT 5
US-09-759-143-878
; Sequence 878, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqun
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
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Db      333  TCCCATCAACAAATATTTTATATAAATTCCTGATCATCAACAAAGCTTGGCAATG 392
Qy      121  ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaIleValGln 140
Db      393  GTTTCATCAGCTCTCTGGSCAATGGTTTAACTGCGCAGGTGTGATACGACAAATTTGTCAA 452
Qy      141  LeuHisAsnGlyThrLysTyrIleValAspHisIstIleuAspLysIstPmeLeuThr 160
Db      453  CTTCAATAAAGGAACCAAGATATAGAAAGTTTCCACATTTGGTTGGATTAAGTGATTTACA 512
Qy      161  ArgLysGlnPheGlyLeuLeuSerPhePheAlaValLeuHisAlaIleTyrSerLeu 180
Db      513  AGAAAGCAGTTTGGGCTTCTCAAGTTTCTTTTGTGCTTACGTCATGCATTAATTTAATCTG 572
Qy      181  SerTyrPromeLarArgSerTyrArgTyrIleLeuLeuAsnIstIstIstIstIstIstIst 200
Db      573  TCTTACCAATAGAGCCGATCTCTACAGATACAAAGTTGGTAACTGGGCGATTAACAGGTC 632
Qy      201  GlnGlnAsnLysGluAspAlaIstIstIleGlnHisAspValIstPargMeGluIleTyrVal 220
Db      633  CAACAAATTAAGAAGATGCTGTGATTTGAGCATGATGTTTGGAGAAATGAGATTTATGCG 692
Qy      221  SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValIstSerIleProSer 240
Db      693  TCTCTGGAAATTTGGGATTTGGCAATATCTGGCTCTGTGCTGTGACATCTATTCATCTCT 752
Qy      241  ValSerAspSerLeuThrIstPargGluPheIstIstIstIstIstIstIstIstIstIst 260
Db      753  GTGAGTGACTTTTGACATGAGAGAAATTTCACTATATTCAGACGAAGTAGAAATTTGTT 812
Qy      261  SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaIstPasnLysIstIleAspIle 280
Db      813  TCCCTTCACTAGGCGCAATACACGATGATTTTGGCTGGAGATTAAGTGAATAGATATA 872
Qy      281  LysGlnPheValIstPtyrThrProPothrPheMetIleAlaValPheLeuProIleVal 300
Db      873  AAACAAATTTGATAGTATACACCTCCAACTTTATATATGCTGTTTCTTCCCAATTTGTT 932
Qy      301  ValLeuIlePheLysSerIleLeuPheLeuProCysLeuAlaArgLysIleLeuLysIle 320
Db      933  GTCTGATATTTTAAACATACATATTCCTGCGCAATGCTTGAAGAAAGAACTACTGAAGATT 992
Qy      321  ArgHisGlyIstIstIstIstIstIstIstIstIstIstIstIstIstIstIstIst 339
Db      993  AGACATGCTTGGGAGACGTCACCAAAATTAACAAACATGAGATATGTTCCAGATTG 1049

RESULT 9
US-09-323-873A-6
; Sequence 6, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Khan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.160SU2
; CURRENT APPLICATION NUMBER: US/09/323,873A
; PRIOR FILING DATE: 1999-06-01
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-09-323-873A-6

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Alignment Scores: 1.17e-150 Length: 3627
 Pred. No.: 1358.50 Matches: 338
 Score: 29.68% Conservative: 0
 Percent Similarity: 29.68% Mismatches: 1
 Best Local Similarity: 75.89% Indels: 801
 Query Match: 3 Gaps: 1
 DB:

US-10-750-262-2 (1-339) x US-09-323-873A-6 (1-3627)

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 Db ATGGAAGACAGAAAAGACATCCAAACAGAAAGAACTTGGAAATGAGCCTAGAGAGA 155
 QY 21 AsnLeuGluGluAspAspTyrLeuHisLysAspTrpGluLysSerMetLeuLysArg 40
 Db AATTAGAAAGAGAGATATTATGCAATAGAGACAGGAGAGACAGCAATGCTAAAGAGA 215
 QY 41 ProValLeuLeuHisLysGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
 Db CCTGGCTTTTGCATTTGACCAACAGCCAGCTGATGAAATTTGACTGCCCTTCAGAA 275
 QY 216 CTTGAGCATCTCTGATTTGACCAACAGCTGATGAAATTTGACTGCCCTTCAGAA 275
 Db 61 LeuGlnHisLeuGlnGluLeuPheProGlnTrpHisLysProLysAlaAlaAlaLe 80
 QY 276 CTTGAGCATCTCTGATTTGACCAACAGCTGATGAAATTTGACTGCCCTTCAGAA 335
 Db 81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
 QY 336 ATAGGATCTCTGATTTTCTTACACTCTCTGAGGAGAAATTAATCACTTACGAACT 395
 Db 101 SerHisGlnGlnTyrPheTyrLysIleProLysLeuValIleAsnLysValLeuProMet 120
 QY 396 TCCCAATCAACAAATATTTATTAATAATTCACATCTGATCAACAAAGCTTGGCCAAAG 455
 Db 121 ValSerLysGThrLeuLeuAlaLeuValTyrLeuProGluValIleAlaAlaLeValGln 140
 QY 456 GTTTTCATCACTCTCTGATTTGATGCTTACCTGCCAGGTGATAGAGCAATTTGCCAA 515
 Db 141 LeuHisAsnGlyThrLysTyrLysLysPheProHisLysTrpLeuAspLysTrpMetLeuThr 160
 QY 516 CTTCAATATGGAACCAAGATTAAGAAATTTCCACATTTGATGATTAAGTGAAGTGAAGTGAACA 575
 Db 161 ArgLysGlnPheGlyLeuLeuSerPhePheAlaValLeuHisAlaIleTyrSerLeu 180
 QY 576 AGAAACGAGTTTGAGCTTCTCAGTTCTTTTGTGCTACTGCATGCAATTTATAGCTG 635
 Db 181 SerTyrProMetArgAspSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
 QY 636 TCTTATCCCAATGAGCGCATCTCAAGATACAAAGTTGCTAAACTGGCATATCAACAGTGC 695
 Db 201 GlnGlnAsnLysGluAspAlaATPILegLHisAspValTrpArgMetGluLysTyrVal 220
 QY 696 CAACAAATTAAGAAAGATGCTGATTTGAGCATGATGTTTGAGAAATGAGAAATTTATGTG 755
 Db 221 SerLeuGlyLysValGlyLeuAlaIleLeuAlaLeuLeuAlaValIleThrSerLysProSer 240
 QY 756 TCTCTGGAAATTTGGAGATTTGGCAATATGCTCTGTTGGCTGTGACATCTATCTCATCT 815
 Db 241 ValSerAspSerLeuTrpArgGluPheHisTyrIle----- 253
 QY 816 GTGAGTACTTTTGACATGAGAGAAATTTCACTATAT-TCAGGTAAATATATATATAAA 874
 Db 253 ----- 253
 QY 875 TAACCTTAAGAGTAATCTTCTTTTGTATTATGATATAGAAATANGTTGACTTTACCC 934
 Db 253 ----- 253
 QY 935 CATAAATAATACAAAATGTTTTTCAACAGCAAAAGCTTTATATCTTTGCAATTAATAAT 994
 Db 253 ----- 253

Db 995 GTGCTCTCTGTTGTTTCCCTATGCTCTAAATTAGACAGAGTTTCCTAGACATMAA 1054
 QY 253 ----- 253
 Db 1055 TAAAGGCATTAATAATATCTTGTGTTTTTTTTTTTGTGTTGTTTGTGTTGTTT 1114
 QY 253 ----- 253
 Db 1115 GTTTGTTTTTTTGAATGAAGTCTCGCTCTGTGCTCCCATGCTGAGTAAGTGGACGAT 1174
 QY 253 ----- 253
 Db 1175 CTGGCTCAGTCGAACCTGCGCTCTGAGTTTCAAGCGATTTCTGTGCTCAGCCTCTG 1234
 QY 253 ----- 253
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 QY 253 ----- 253
 Db 1295 GACAGGTTTTTCCATGTTGGCCAGGCTGCTGATCTCGATCTCGAATCGAATGATCGGC 1354
 QY 253 ----- 253
 Db 1355 CACCTGGCCTCCCAAGTGTGGATGACAGTTGTAGCCACACACTCAGCCTGCTCT 1414
 QY 253 ----- 253
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 QY 253 ----- 253
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QY 253 ----- 253
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 QY 253 ----- 253
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 QY 253 ----- 253
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 QY 253 ----- 253
 Db 3035 ATTTGTTCCTTAGACAGCTTGAGACAAAGAAATTAACCAAAAGTAAGTGAAGAGAT 3094
 QY 253 ----- 253
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 QY 253 ----- 253
 Db 3155 CATAGATTAAGATTTCCAAAGCAAGAGCATATCCAGATGAGTAGATGGGATTAAGT 3214

QY 254 ----- GlnSerIysLeuGlyIleVal 260
 Db 3215 CTTATTGAACCAATCTTCAACCAATTTGTTTTCTTTTGGAGAGCAAGCTAGGAATTTGTT 3274
 QY 261 SerIleuLeuGlyThrIleHisAlaLeuIlePheAlaIlePheAspIle 280
 Db 3275 TCCCTTCTACTGGGACCAATACACGATTTGTTTCCCTGGAGATAGGATAGATATA 3334
 QY 281 LysGlnPheValIlePheIleThrProPheIlePheMetIleAlaValPheLeuProIleVal 330
 Db 3335 AAACAATTTGATGTATGATACCTCACTTATATAGCTGTTTCTTCCATTTGTT 3394
 QY 301 ValIleuIlePheIleSerIleLeuPheLeuProGlyLeuArgIleValIleLeuIle 320
 Db 3395 GTCCGATATTTTAAAGCAATCTATTTCTGCGATGCTTGAGAGAAAGATAGTGAAGATT 3454
 QY 321 ArgHisGlyTrpGlyAspValThrIleValIleAspIleValIleGlySerGlnLeu 339
 Db 3455 AGCAATGTTGGGAAGAGCTCAACAAATTTACAAATGAGATATGTTCCAGTTG 3511
 RESULT 10
 US-09-455-486-4
 ; Sequence 4, Application US/09455486
 ; Patent No. 6833438
 ; GENERAL INFORMATION:
 ; APPLICANT: Daniel E. Afar
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Douglas C. Saffran
 ; APPLICANT: Stephen C. Mitchell
 ; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
 ; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
 ; FILE REFERENCE: 129.17-US-11
 ; CURRENT FILING DATE: US/09/455,486
 ; PRIOR FILING DATE: 1999-12-06
 ; PRIOR APPLICATION NUMBER: 09/323,873
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 3627
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-455-486-4
 Alignment Scores:
 Pred. No.: 1,17e-150 Length: 3627
 Score: 1358.50 Matches: 338
 Percent Similarity: 29.68% Conservative: 0
 Best Local Similarity: 29.68% Mismatches: 1
 Query Match: 75.89% Indels: 801
 DB: 3 Gaps: 1
 US-10-750-262-2 (1-339) x US-09-455-486-4 (1-3627)
 QY 1 MetGluSerArgIleAspIleThrAsnGlnGluLeuTrpIleMetIleProArg 20
 Db 96 ATGAAAGCAGAAAGACATCAACAAACCAAGAACTTTGGAAATGAAGCTTAGAGAG 155
 QY 21 AsnLeuGlnGluAspArgIleLeuHisIleAspThrGlyIleThrSerMetLeuIleVal 40
 Db 156 AATTAGAAAGAGACATTAATTTGCAATTAAGGACACGAGAGACGACATGCTTAAGAA 215
 QY 41 ProValLeuLeuHisIleuHisGlnThrAlaHisAlaAspGluPheAspProGly 60
 Db 216 CCGTCTTTTGCATTTGACCAACAAAGCCATGCTGATGAATTTGACGCTTCAGAA 275
 QY 61 LeuGlnHisThrGlnGluLeuPheProGlnTrpHisIleuProIleValIleAlaIle 80
 Db 276 CTTTCAGACACACAGAACTTTTCCACAGTGCATTCGCAATTAATTAAGTCTGCTATT 335
 QY 81 IleAlaSerLeuThrPheLeuTrpThrIleuLeuArgIleValIleHisProLeuAlaThr 100

Db 336 ATAGACATCTGACCTTTCTTTACACTCTCTGAGGAGATATTCACCCCTTAGCAACT 395
QY 101 SerHesgInglInYrPheTyLysIleProIleLeuValIleAenLysValLeuProMet 120
Db 396 TCCATCAACAATATTTTATATAATCCAACTCGGATCCAAAGAAAGCTTGGCAATG 455
QY 121 ValSerIleThrLeuLeuAlaLeuValTyLeuProGluValIleAlaIleValGln 140
Db 456 GTTTCATCACCTCTCTGGCATGGTTTACCTGCCAGGTTGATGACGCAATTTCCAA 515
QY 141 LeuHsaAngLYThrLysTyLysLysPheProHsITrPLeuAspLysTrpMetLeuThr 160
Db 516 CTTCTAATGAAACCAAGATATAAGATTTCCACATGGTTGATGATGAGATGTTAAACA 575
QY 161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHsAlaIleTySerLeu 180
Db 576 AGAAGACAGTTGGGCTCTCAGTTCTTTTGGCTGTACTGCATGCAATTTATAGTCTG 635
QY 181 SerTyrrPrometArgArgSerTyrrArgTyLysLeuLeuAsnTrpAlaTyGlnGlnVal 200
Db 636 TCTTACCCCATAGAGGCGATCTCAAGATACAGATTCCTAACTGGGCAATACACAGCTC 695
QY 201 GlnGlnAenLysGlnAspAlaTrpIleGlnHsAspValTrpArgMetGluIleTyVal 220
Db 696 CAACAAAATRAAGAGATCCCTGGATTTGAGCATGATGTTGGAGATGAGATTTATGTG 755
QY 221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
Db 756 TCTCTGGGAATGTGGGATTTGGCAATACCTGGCTCTGTGGCTGTGACATCTATTTCACTC 815
QY 241 ValSerAspSerLeuThrTrpArgGlnPheHsTyLle----- 253
Db 816 GTGAGTACTCTTTGACATGAGAGAAATTCACCTAAT-TCAGGTAAATATATATATAA 874
QY 253 ----- 253
Db 875 TAACTTAAGAGTAATCTCTTTTGTGTTATGATATAGATATGTTGACTTAAACC 934
QY 253 ----- 253
Db 935 CATAAAAAATACAAATGTTTTTCAACAGCAAGATCTTACTGTTCCAAATTAATAT 994
QY 253 ----- 253
Db 995 GTGCTCTCTGTTGTTTCCCTATGCTTCTAATTAGACAAGTGTTCCTAGACATAAA 1054
QY 253 ----- 253
Db 1055 TAAAAAGCATTAATAATCTTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1114
QY 253 ----- 253
Db 1115 GTTTGTTTTTTAGATGAAGTCTCGCTGTGTGCCATGTGAGTAGACGTGGCAGAT 1174
QY 253 ----- 253
Db 1175 CTCGGCTCACTCAACCTGCGCTCTGGGTTCAAGGCAATTCCTTGCTCAGCCTCTG 1234
QY 253 ----- 253
Db 1235 AGTAGCTGGGATTACAGGACCCCATCACCATGTCAGCTAATTTTTGTATTTTAGTAGA 1294
QY 253 ----- 253
Db 1295 GACAGGGTTTTCCATGTTGGCAGGCTGTCTCGATCTCTGAACCTCAATGATCCGCC 1354
QY 253 ----- 253
Db 1355 CACCTCGGCTCCCAAGTGTGGGATGACAGTGTGAGCCACACACTCAGCCTGCTCT 1414
QY 253 ----- 253
Db 1415 TTCTAATATTTTGAACCTTGTTAGACAATTTGCTACCCATCTAATGTGATATTTTAGAAT 1474

QY 253 ----- 253
Db 1475 CCAATATGATGATGTTATTTATTTCTTAAAAAAATATTTCTTTTACCTGTCACTGAATTT 1534
QY 253 ----- 253
Db 1535 AGTAATGCTTTTATGTTTACCAAACTTAGACCTTCCGAAACAAAACCTCTCTCTGA 1594
QY 253 ----- 253
Db 1595 AATAATAGTTTTTATCTACCAAAAGATATGCTAGTGTCTCATTTCAAAAGCTGCTTTT 1654
QY 253 ----- 253
Db 1655 CCAGCTACATTTTATATATATCTACTCACTGAAGTTCTAAATATTTCTGTATTTTAAA 1714
QY 253 ----- 253
Db 1715 ACTATCTAGATTTTACTGAGGTTTATCTTCTGTGTAGATTTATTCATAAGAGATGAT 1774
QY 253 ----- 253
Db 1775 GTCCAGAAATCACTCGGGATCTGTCTGACAAAGATTCAAAGACTAAATTTAATTCAG 1834
QY 253 ----- 253
Db 1835 TCATGAACACTGCCAATTAACGTTTATGGTAGACATCTTTGAAATTTCCAAAGTCA 1894
QY 253 ----- 253
Db 1895 GACATTCGCACTATCCCTTCTACATGTCACACGATATCTCCAACTTTATTAGGAT 1954
QY 253 ----- 253
Db 1955 CTGATTAGTTGAAAGTATGCTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGTA 2014
QY 253 ----- 253
Db 2015 CAACATTCACAGAAATTCCTAATTTTGTAGTTGAGCTGATTAACCTGAGTTCTT 2074
QY 253 ----- 253
Db 2075 TGTCTCTAATTAATAGCTTTCTTCAACATGCTCTGCTGTTAGACATATGATGAACA 2134
QY 253 ----- 253
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QY 253 ----- 253
Db 2195 TATATGTACAATCTAGCCCATATAGTATACATACATTTGGTAAACTAATTTT 2254
QY 253 ----- 253
Db 2255 CAACCAATGACATGATTTTTCAACTAGTAACTAGAAATGTTCACTTAAAAATCTGAGA 2314
QY 253 ----- 253
Db 2315 ACTGTGTACACTACAATTACTTGAGATTCAATATGAAAACGCAAACTTAGCTATTT 2374
QY 253 ----- 253
Db 2375 GATTGTATTCACGTGGACTTAAGATGCGCTGATATATGTGATGATTGCTTCTGG 2434
QY 253 ----- 253
Db 2435 CAGGCTAATGACATTTCCAGTAAAGTATAGAGTICAGAAGTCTATATAAGAGGTGT 2494
QY 253 ----- 253
Db 2495 TGTCAAGAACCGTTGAGATTACATAGGTGAACAATATTTTAAAGCACTTATTTGTG 2554


```

; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappel
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 511582001601
; CURRENT APPLICATION NUMBER: US/10/010,667A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-667A-6

Alignment Scores:
Pred. No.:      1,17e-150          Length:      3627
Score:         1358.50           Matches:     338
Percent Similarity: 29.68%       Conservative: 0
Best Local Similarity: 29.68%    Mismatches:  1
Query Match:   75.89%           Indels:     801
DB:                                     Gaps:        1

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QY      21 AsnLeuGlnGluAspSprTyrLeuHislyrAspThrGlyCylThrSerMetLeuLysArg 40
Db      156 AATTTAAGAAAGAACACATTATTGTTCATAAGGACACCGGAGAGACCAGCATGTATAAAAGA 215
QY      41 ProValLeuLeuHisIleuHisgInThrAlaHisAlaAsnGluPhaAspCySProSerGlu 60
Db      216 CCTGCCTTTTGCCATTTTGCACCAACAGGCCACGCGAAGAAATTGACATGCCCCCTTCAGAA 275
QY      61 LeuGlnHsrThrGlnGluLeuPheProGlnTPHisIeuProIleLysIleAlaIle 80
Db      276 CTTCAGCACACACAGGAACCTTTCCACAGTGGCACTTCCATTAAATAGCTGCTAAT 335
QY      81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
Db      336 ATAGCATCTCGACCTTTCTTACACTCTTCGAGGAAAGTAATTCACCCCTTAGCAACT 395
QY      101 SerHisgInTyrPheTyrTyrIleProIleLeuValIleAsnLysValLeuProMet 120
Db      396 TCCCATCAACAAATATTTTTATTAATAATTCMAATCCGTCATCAACAAAGTCTTGGCCAATG 455
QY      121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlnValIleAlaAlaIleValGln 140
Db      456 GTTTCATCACACTCTCTTGGCATGTGTTTAACTCGCAGGATGATAGACGCAATTTGCCAA 515
QY      141 LeuHisAsnGlyThrLysTyrLysLysPheProHisTyrPLeuAspLysTyrMetLeuThr 160
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QY      161 ArgLysGlnPheGlyLeuLeuSerPhePheHealValIleuHisAlaIleTyISerLeu 180
Db      576 AGAAAGCAGTTTGAGCTTCTCAGTTTTCTTTTGTCTACGTCATGACCAATTAATAGTCTG 635
QY      181 SetTyrProMetAcGASerTyrArgTyrLysLeuLeuAsnTPalaTyGlnGlnVal 200
Db      636 TCCTAACCAATAGAGGCAATCTCAAGATACAAAGTTGCTTAACTGGGCAATATCAACAGGTC 695
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Oy 241 ValSerAspSerLeuThrThrPheGluPheHisTyrIle 253
Db 816 GTGAGTACTCTTGTACATGAGAGAAATTCCTATAT-TCAGGTAATATATATATAA 874
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Db 935 CATAAAAATATACAATGTTTTCAACAGCAAGAATCTTATATCTTGTCCAATTATATAT 994
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Oy 253 ----- 253
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Oy 253 ----- 253
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Db 2195 TATATGTACAATACCTAGCCCATTAATAGGTATACATACACTTGTGTAATAATTTT 2254
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Db 2315 ACTGTTACATCAAGTAACTTACCTGGAGATTCATATATGAAAAAGCAACTTAGCTATT 2374
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Db 2495 TGTCAAGACCGTTGAGATTACATAGTGAACAACTATTTTAAAGCACTTATTTGTG 2554
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Db 2555 TAGTGAACAAGCATCCCAATGACAGGCTGAATGTTTCATCAATCTGTGATCTCTAT 2614
Oy 253 ----- 253
Db 2615 TTTGTGACATTTGAAAAAATGTTCTATATTTTCCATGTTATGAAATATTTGATTT 2674
Oy 253 ----- 253
Db 2675 TTTAAAAACATPAGCCAAAGTTCACTTCATTCACTTATTCATTATTCAAATCAGAGTGAT 2734
Oy 253 ----- 253
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Oy 253 ----- 253
Db 2795 TCTTCAATCTAATATTTATTTATGAGAAATCTAATAATGTAACAATCATGTGTGATTC 2854
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Db 2855 GCAATGATCTGTATAAGTAAGACTGATCCGATTTAGGTATCTGTGAAGACAG 2914

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QY 253 ----- 253
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QY 253 ----- 253
Db 3035 ATTTGTCTTACCTTACAGACCTTGAGAGACAAAGAAATTAACCAAAAGTAGGTGAGAGAT 3094
QY 253 ----- 253
Db 3095 AGGCAAAAAGAGACAAAGATGTGATGACATTTGTTGAGAAATGTGATGAGAAAAAAT 3154
QY 253 ----- 253
Db 3155 CATGATAAAGAGATTTCCAGACAGACATATCCAGATGAGTAGAGTGAATTAAC 3214
QY 254 ----- GlnSerLysLeuGlyLeuVal 260
Db 3215 CTTATTTGAACCATCTTACCAATTTTGTCTTTTTCAGAGACAGAGCTAGAGAAATGTT 3274
QY 261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaIlePheAlaIlePheAlaIle 280
Db 3275 TCCCTTCTACTGGGACAAATACACCATTTGCTGCTGAGAAATGAGTGAATGATATA 3334
QY 261 LysGlnPheValIlePheThrProThrPheMetIleAlaValPheLeuProIleVal 300
Db 3335 AAACAATTTGATGTATACACCTCACTTTATGATAGCTTTCTTCCATTTGTT 3394
QY 301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuGlyLysIleLeuLysIle 320
Db 3395 GTCCGATATTTAAAGCATCTATCTGCGCATGCTGAGAGAAATATCTGAAAGATT 3454
QY 321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
Db 3455 AGACATGGTGGGAAGAGTCAACCAAAATTAACAAACTGAGATATGTTCCAGTTG 3511

RESULT 12

US-09-949-016-14428
Sequence 14428, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949, 016
PRIOR FILING DATE: 2000-04-14/755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PaeSeq for Windows Version 4.0
SEQ ID NO 14428
LENGTH: 9073
TYPE: DNA
ORGANISM: Human
US-09-949-016-14428

Alignment Scores:

Pred. No.: 6,24e-116 Length: 9073
Score: 1071.50 Matches: 309
Percent Similarity: 23.59% Conservative: 0
Beet Local Similarity: 23.59% Mismatches: 2
Query Match: 59.86% Indels: 1000
Gaps: 2

US-10-750-262-2 (1-339) x US-09-949-016-14428 (1-9073)
QY 29 HisLysAspThrGlyGluThrSerMetLeuLysArgProValIleLeuHisIleHisGln 48
Db 3049 CATTAAGACACGGGAGAGACCGAGCATGCTAAATAAGCTGTGCTTTGATTTGCAGCAA 3108
QY 49 ThrAlaHisAlaAspGluPheAspCysProSerGluLeuGlnHisThrGlnIlePhe 68
Db 3109 ACAGCCCACTGATGAATTTGATGCTGCCCTTCAGAACTTCACACACAGGAACTCTT 3168
QY 69 ProGlnTrpHisLeuProIleLysIleAlaIleIleAlaSerLeuThrPheLeuTrp 88
Db 3169 CCACAGTGCATTTCCCAATTAATAATGCTGATTAATGACATCTCTGATCTTTCTTAC 3228
QY 89 ThrLeuLysArgGluValIleHisProLeuAlaThrSerHisGlnGlnIleTrpPheTrp 108
Db 3229 ACTCTTCTGAGGAGATTAATTCACCTTTAGAACTTCCATCAACATATTTTATATA 3288
QY 109 IleProIleLeuValIleAsnLysValLeuProMetValSerIleThrLeuAlaLeu 128
Db 3289 ATTCCAATCTGGTCATCAACAAAGCTTGGCAATGTTCCATCATCTCTTGGCATTTG 3348
QY 129 ValTrpLeuProGlyValIleAlaAlaIleValGlnLeuHisAsnGlyThrLysTrpLys 148
Db 3349 GTTTACCTGCGCAGGTGTATAGCAGCAATTTGTCCAACTTCAATAGAAACCAAGTATAG 3408
QY 149 LysPheProHisTrpLeuAspLysTrpMetLeuThrArgLysGlnPheGlyLeuLeuSer 168
Db 3409 AAGTTTCCACATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3468
QY 169 PhePhePheAlaValLeuHisAlaIleTrpSerLeuSerTrpPrometArgArgSerTrp 188
Db 3469 TTTCTTTTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3528
QY 189 ArgTrpLysLeuLeuAsnTrpAlaTrpGlnIleVal----- 200
Db 3529 AGATACAGTTGCTTAACTGGCATATCAACAGGT-AAAGTACAGTTGTGACACTGTTA 3587
QY 200 ----- 200
Db 3588 CTAAATAAAAGTCTAAGTCACTCAACAAATTAATCATTTGCTGATTAATCAATACC 3647
QY 200 ----- 200
Db 3648 CAACCTGTTGAACCTGTGTGTAAGAAAGTCACTATTTAAATTTTATTATTAATTA 3707
QY 200 ----- 200
Db 3708 CACTAGGCTTGTGTGCTGCTGCTGTTTATATGAGAAATGTTTGTAGCTGAAATAA 3767
QY 200 ----- 200
Db 3768 GTTACAACCTTAGCAACATAGAAACATTTTGTTCATGACGAGGCCATATTTCAAACTT 3827
QY 200 ----- 200
Db 3828 CTACCACTTCACAGATTAATTTTAATATGTGTGTCTTCTGTTTACCAATATAG 3887
QY 200 ----- 200
Db 3888 CATGCACTTACAGTTCTATTCAGATTAACATCAATATTAATTAAGAAATTAATAGAT 3947
QY 200 ----- 200
Db 3948 TATGAAAGTGTTCATTTCAAGAAAAAAGTATGATGCTCTATGTCTATTTGTTAGAGA 4007
QY 200 ----- 200
Db 4008 ATGCAAAAAAAGAAAGAAAGTATTAATTTGTGAGACCTGTTATCAGGCTTCAT 4067
QY 200 ----- 200
Db 4068 AGTAGCAGAGGAGAGAGTGAAGAGATTCACATTCAGAGAAATTAATCTGTTTGTGCA 4127


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; ORGANISM: Homo sapien
US-09-439-313-342

Alignment Scores:
Pred. No.: 5,62e-98      Length: 592
Score: 905.00           Matches: 171
Percent Similarity: 99.42%  Conservative: 0
Best local Similarity: 99.42%  Mismatches: 1
Query Match: 50.56%       Indels: 0
DB: 3                      Gaps: 0

US-10-750-262-2 (1-339) x US-09-439-313-342 (1-592)

QY      1  MetGISeRrArgLySaApIleThrAsnGIGLInLueUtrPlySmelYsPfoARgArg 20
Db      518 ATGAAAGCGAGAAAGACATCAACAACCAAGAAACCTTTGGAAAAAGAGCTTAGGAGA 458
QY      21  AsnLueGInLubSaPpTYrLueuHieLyAsPthrgLYGInuThrSeRmeLueLyArg 40
Db      458 AATTAGAGAGAGCGATTATTTCGATNAGAGACGGGAGAGACGACACGATCTTAAAAAGA 399
QY      41  ProValLueuHieLueuHieGInThrAlaHieAlaSpLubPheAPCyProSeRgLu 60
Db      398 CCGTGTGTTTGGATTGGACCAACAGCCCATGCTGATGAATTGACTGCCCTTCGAA 333
QY      61  LeuGInHieThrgInLueuPheProGInThrHieLueuArgLuvAlIleHiePProLueuAlaThr 80
Db      338 CTTACAGCACACAGAACTCTTCCACAGTGGACACTGCCAATTAAAAATAGCGCTATT 279
QY      81  IleAlSeRleuThrPheLueuTYrThrLueuArgLuvAlIleHiePProLueuAlaThr 100
Db      278 ATAGCATCTCTGACTTTCTTTACACTCTTCTGAGGAAGTAATCACTTTAGCACT 219
QY      101 SerHieGInLueuThrPheTYrLysIleProIleLueuAlIleAsnLyValLueuProMet 120
Db      218 TCCCAACCAAAATATTTTATATAAATTCACATCTGTCATCAACAAAGCTTGGCAATG 159
QY      121 ValSeRleThLueuLueuAlLueuValTYrLueuProGInYValIleAlaAlIleValGIn 140
Db      158 GTTTCATCATCTCTCTTGGCATTTGGTTTACCTGCCAGGATGATAGCACCAATTGTCCAA 99
QY      141 LeuHieAsnGlyThrLysTYrLysLysPheProHieSTRPLeuAspLysTRPmeLueuThr 160
Db      98 CTTCAATATGGAACCAAGATAGAAAGTTTCCACATCTGTTGATAGTGAATGATTAAACA 39
QY      161 ArgLySeGInPheGlyLueuLueSerPhePheAla 172
Db      38 AGAAAGCAATTTGGCTTCTCAGTTCTTTTGGCT 3

RESULT 14
US-09-352-616A-342/C
; Sequence 342. Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiengchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.42708
; CURRENT APPLICATION NUMBER: US/09/352,616A
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-342

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Pred. No.: 5,62e-98 Length: 592
Score: 905.00 Matches: 171
Percent Similarity: 99.42% Conservative: 0
Best Local Similarity: 99.42% Mismatches: 1
Query Match: 50.56% Indels: 0
DB: 3 Gaps: 0

US-10-750-262-2 (1-339) x US-09-352-616A-342 (1-592)

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DB 518 ATGAAAGCAAGAAAGACATCAAAACCAAGAAAGACTTTGGAAAAATGAAGCTTAGAGAGA 459
QY 21 AsnLeuGIuGIuAspAspTrpLeuHlslyAspTrpGIuGIuThSerMetLeuLyArg 40
DB 458 AATTAGAAAGAAAGACATTAATTGCAATAGAAACAGGAGAGACAGACATGCTTAAGAA 399
QY 41 ProValLeuLeuHlsleuHlsGInThraHlsAlaAspGIuPheAspCyseProseGIu 60
DB 398 CCGTGCTTTTCATTTGACCAACCAAGCCCAATGCTGATGAATTTGACCTGCCCTTCAGAA 339
QY 61 LeuGIuHlsThrGIuLeuPheProGIuTrpHlsleuArgGIuValHlsProleuAlaThr 80
DB 338 CTTGACGACACACAGGAACCTTTCCACAGTGCACCTGCCAATTAATAAGCTGCTATT 279
QY 81 IleAlaSerLeuThrPheLeuTrpThraLeuArgGIuValHlsProleuAlaThr 100
DB 278 ATAGCATCTCTGACTTTCTTAACACTCTTGAGGAAAGTAATTCACCTTAGCAACT 219
QY 101 SerHlsGInGIuTrpPheTrpLyHlsleuValHlsAsnLyValLeuPromet 120
DB 218 TCCCATCAACAAATATTTTATTAATTCCAATCTGGTATCAACAAAGCTTGCAAAATG 159
QY 121 ValSerIleThrLeuLeuAlaLeuValTrpLeuProGIuValHlsAlaIleValGln 140
DB 158 GTTTCATCACTCTCTTGCAATGGTTTACCTGCCAGTGTGATGACGAATTTGCCAA 99
QY 141 LeuHlsAsnGIuThrLyTrpLyHlsPheProHlsTrpLeuAspLySTrMetLeuThr 160
DB 98 CTTCAATATGAAACCAAGTATAGAAATTTCCACATTTGGATAGTGAATGATTTAACA 39
QY 161 ArgLyGInPheGlyLeuLeuSerPhePheAla 172
DB 38 AGAAAGCARATTTGGGCTTCTCAGTTCTTTTGGCT 3

RESULT 15
; Sequence 342, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
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SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-342

Alignment Scores:

Pred. No.: 5,62e-98 Length: 592
Score: 905.00 Matches: 171
Percent Similarity: 99.42% Conservative: 0
Best Local Similarity: 99.42% Mismatches: 1
Query Match: 50.56% Indels: 0
DB: 3 Gaps: 0

US-10-750-262-2 (1-339) x US-09-636-215-342 (1-592)

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DB 518 ATGAAAGCAAGAAAGACATCAAAACCAAGAAAGACTTTGGAAAAATGAAGCTTAGAGAGA 459
QY 21 AsnLeuGIuGIuAspAspTrpLeuHlslyAspTrpGIuGIuThSerMetLeuLyArg 40
DB 458 AATTAGAAAGAAAGACATTAATTGCAATAGAAACAGGAGAGACAGACATGCTTAAGAA 399
QY 41 ProValLeuLeuHlsleuHlsGInThraHlsAlaAspGIuPheAspCyseProseGIu 60
DB 398 CCGTGCTTTTCATTTGACCAACCAAGCCCAATGCTGATGAATTTGACCTGCCCTTCAGAA 339
QY 61 LeuGIuHlsThrGIuLeuPheProGIuTrpHlsleuArgGIuValHlsProleuAlaThr 80
DB 338 CTTGACGACACACAGGAACCTTTCCACAGTGCACCTGCCAATTAATAAGCTGCTATT 279
QY 81 IleAlaSerLeuThrPheLeuTrpThraLeuArgGIuValHlsProleuAlaThr 100
DB 278 ATAGCATCTCTGACTTTCTTAACACTCTTGAGGAAAGTAATTCACCTTAGCAACT 219
QY 101 SerHlsGInGIuTrpPheTrpLyHlsleuValHlsAsnLyValLeuPromet 120
DB 218 TCCCATCAACAAATATTTTATTAATTCCAATCTGGTATCAACAAAGCTTGCCAAATG 159
QY 121 ValSerIleThrLeuLeuAlaLeuValTrpLeuProGIuValHlsAlaIleValGln 140
DB 158 GTTTCATCACTCTCTTGCAATGGTTTACCTGCCAGTGTGATGACGAATTTGCCAA 99
QY 141 LeuHlsAsnGIuThrLyTrpLyHlsPheProHlsTrpLeuAspLySTrMetLeuThr 160
DB 98 CTTCAATATGAAACCAAGTATAGAAATTTCCACATTTGGATAGTGAATGATTTAACA 39
QY 161 ArgLyGInPheGlyLeuLeuSerPhePheAla 172
DB 38 AGAAAGCARATTTGGGCTTCTCAGTTCTTTTGGCT 3
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Search completed: December 6, 2005, 18:45:28
Job time : 231 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 03:12:22 ; Search time 320.456 Seconds
(without alignments)
987.688 Million cell updates/sec

Title: US-10-750-262-1_COPY_66_1082
Perfect score: 1017
Sequence: 1 atggaagcagaagaacat.....ctgagatgtccacgtg 1017

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3289935 seqs, 155610033 residues

Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_New:
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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB_seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	39.2	3.9	1779	6	US-10-750-185-25365 Sequence 25365, A
2	37.2	3.7	2464	6	US-10-750-185-39315 Sequence 39315, A
3	36	3.5	872	6	US-10-750-185-49060 Sequence 49060, A
4	34.2	3.4	1012	6	US-10-750-185-54610 Sequence 54610, A
5	34.2	3.4	3609	6	US-10-750-185-63875 Sequence 63875, A
6	34	3.3	1240	6	US-10-750-185-10880 Sequence 30880, A
7	33.8	3.3	1458	6	US-10-821-234-142 Sequence 142, App
8	33.8	3.3	2748	6	US-10-750-185-48714 Sequence 48714, A
9	33.4	3.3	1840	6	US-10-750-185-18552 Sequence 38532, A
10	33.2	3.3	973	6	US-10-750-185-55233 Sequence 35293, A
11	33.2	3.3	340000	7	US-11-108-172-547 Sequence 547, App1
12	32.8	3.2	1135	6	US-10-750-185-58068 Sequence 58068, A
13	32.8	3.2	1135	6	US-10-750-185-54184 Sequence 54184, A
14	32.8	3.2	1765	6	US-10-750-185-54184 Sequence 54184, A
15	32.4	3.2	1307	6	US-10-986-501-27 Sequence 27, App1
16	32.4	3.2	1993	6	US-10-750-185-54772 Sequence 54772, A
17	32.2	3.2	1257	6	US-10-750-185-64012 Sequence 64012, A
18	32.2	3.2	1454	6	US-10-750-185-64704 Sequence 46704, A
19	32	3.1	1252	6	US-10-750-185-62619 Sequence 62619, A
20	32	3.1	3310	6	US-10-750-185-24645 Sequence 24645, A
21	32	3.1	4753	6	US-10-750-185-33545 Sequence 33545, A
22	31.8	3.1	1370	6	US-10-750-185-57153 Sequence 57153, A
23	31.8	3.1	1986	6	US-10-793-626-273 Sequence 273, App

24	31.8	3.1	3043	6	US-10-793-626-3478 Sequence 3478, Ap
25	31.8	3.1	3165	6	US-10-793-626-3360 Sequence 3360, Ap
26	31.8	3.1	3206	6	US-10-750-185-47856 Sequence 47856, A
27	31.8	3.1	3636	6	US-10-793-626-4179 Sequence 4179, Ap
28	31.8	3.1	4168	6	US-10-793-626-4023 Sequence 4023, Ap
29	31.6	3.1	1166	6	US-10-750-185-38045 Sequence 38045, A
30	31.6	3.1	1830	6	US-10-750-185-39246 Sequence 39246, A
31	31.6	3.1	1838	6	US-10-750-185-52241 Sequence 52241, A
32	31.6	3.1	3001	7	US-11-145-703-175 Sequence 175, App
33	31.6	3.1	3001	7	US-11-145-703-176 Sequence 176, App
34	31.6	3.1	150491	7	US-11-112-908-46 Sequence 46, App1
35	31.4	3.1	600	6	US-10-750-185-1485 Sequence 1485, Ap
36	31.4	3.1	1407	6	US-10-750-185-44414 Sequence 44414, A
37	31.4	3.1	1637	6	US-10-750-185-26752 Sequence 26752, A
38	31.4	3.1	2205	6	US-10-750-185-27481 Sequence 27481, A
39	31.4	3.1	4176	6	US-10-793-626-4262 Sequence 4262, Ap
40	31.4	3.1	149419	7	US-11-112-908-47 Sequence 47, App1
41	31.4	3.1	166111	7	US-11-112-908-48 Sequence 48, App1
42	31.2	3.1	1123	6	US-10-750-185-64609 Sequence 54609, A
43	31.2	3.1	1621	6	US-10-750-185-63586 Sequence 63586, A
44	31.2	3.1	2968	6	US-10-750-185-30138 Sequence 30138, A
45	31.2	3.1	3194	6	US-10-750-185-48072 Sequence 48072, A

ALIGNMENTS

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RESULT 1
US-10-750-185-25365
; Sequence 25365, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OR INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25365
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Bovine 19866880604913
US-10-750-185-25365

Query Match 3.9%; Score 39.2; DB 6; Length 1779;
Best Local Similarity 54.1%; Pred. No. 0.1;
Matches 80; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 704 TGACATCTATTCATCTGAGAGTCTTGATGATGAGAGAAATTCATATTCAGA 763
    |||||
DB 765 TGACATTAATTCGTCGTGATGATCTTACTGATCGGCTTAATATATCATTA 824
    |||||
QY 764 GCAAGCTAGGAATGTTCCCTTCACTAGGACAAATACGCAATGATTTTGGCTGGA 823
    |||||
DB 825 AAAGCAGATGACACTTACGCTTTCGTGCGAAATTAAGATTAATGATTTGCTTTGT 884
    |||||
QY 824 ATAAAGTATGATGATTAATTAATTAATTAATGATTTGT 851
    |||||
DB 885 TAACCTATATTTTAAATAAACAATGTTGT 912
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RESULT 2
US-10-750-185-39315/c
; Sequence 39315, Application US/10750185
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
PRIOR FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19315
LENGTH: 2464
TYPE: DNA
ORGANISM: Bovine 19866881564211
US-10-750-185-39315
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Query Match 3.7%; Score 37.2; DB 6; Length 2464;
Best Local Similarity 50.6%; Pred. No. 0.48;
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
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QY 834 AGATATAAAACATTTGTATGTATACACCTCCACCTTTATGATGCTGTTTCTCTCC 893
DB 1748 AGAGAAAGGAAATTTCTGAAATATATAAATGCCATTTGAGATATCTGACATCTTCAT 1689
QY 894 AATGTTGCTCGATATTTAAAGCACTACTATTTCTGCCATGCTTGAGAGAAAGATPACT 953
DB 1688 AACAGACAGCATGATAATTTGCTCTCTCTCTCTATTAATAGTAAGAAAGAAAGAA 1629
QY 954 GAAGATTAGACATGTTGGAGAGCGTCCCAAAATTAACAAACGAGATATGTTCC 1011
DB 1628 CAAGATGTTAAACGTGGGTAAAGAAATCAATTAATAAAACAAACAAACACATGTTTCC 1571
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RESULT 3
US-10-750-185-49060
Sequence 49060, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
PRIOR FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 49060
LENGTH: 872
TYPE: DNA
ORGANISM: Bovine 19866881284640
US-10-750-185-49060
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Query Match 3.5%; Score 36; DB 6; Length 872;
Best Local Similarity 51.9%; Pred. No. 0.61;
Matches 81; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
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DB 57 TATCTTCTTATCCAAACCCACCTCCAACTCTTCCATTTATTTTCATTGAG 116
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QY 376 TTGGCATGTTTACCTGCGAGGTGTATAGACAAATGTCCAACTCATATGAGACC 435
DB 117 TTTATTTCCATTTTCCACTCCAGTACTAGTAATTTGAGATTGTAAGTAACC 176
QY 436 AAGTAAAGAGTTTCCATGTTGTTGATTAAGTG 471
DB 177 AAAATAGAGAGTTGGAAATGCTTATTTGCTGG 212
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RESULT 4
US-10-750-185-54610
Sequence 54610, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
PRIOR FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 54610
LENGTH: 1012
TYPE: DNA
ORGANISM: Bovine 19866881259787
US-10-750-185-54610
```

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Query Match 3.4%; Score 34.2; DB 6; Length 1012;
Best Local Similarity 54.3%; Pred. No. 2.2;
Matches 69; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
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QY 235 GCTATTTATGATCTGCTGACTTTTACACTCTTTCGAGGGAATATTCACCTTTA 294
DB 237 GGAATTAACCAACCAACATTTCTTTATCTTCACTTGAAGTGTACATGACTTTT 296
QY 295 GCACTTCCATCAACAATATTTTAAATTCGAATCTGTCATCAACAAGCTTGG 354
DB 297 AAAAATTTAGATGAATTAATTTTGAAGAGTTTCACTTAAGAGATTAATAAAGACATC 356
QY 355 CCAATGG 361
DB 357 ACAATGG 363
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RESULT 5
US-10-750-185-63875/c
Sequence 63875, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
PRIOR FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
```



```

; SEQ ID NO 63875
;
; LENGTH: 3609
;
; TYPE: DNA
; ORGANISM: Bovine
; -
US-10-750-185-63875
19866880579152

```

Query Match	3.4%	Score 34.2;	DB 6;	Length 3609;
Best Local Similarity	58.3%;	Pred. No. 4.5;		
Matches 60;	Conservative 0;	Mismatches 43;	Indels 0;	Gaps 0;

237 TATTTAGCATCTGTGACTTTTCTTAACCTCTTGAGGGAAGTAATCACCCCTTAGC 296
||||| ||||| |
1979 TAATTAAAGCATTTTCAAATTACTTCACAGTCTTTTAAGATCATCAATTAAATTGCTGCAT 1920

297 AACTTCCCATCACAATATTTTATAAAATTCCAATCTGTC 339
||| ||| ||| ||| ||| ||| ||| |||
1919 AACATTCCATGAAGAAATGTTTTTAACCTTACATAAGCATGTC 1877

RESULT 6
US-10-750-185-30880
Sequence 30880 Amplification HS/10750185

```

sequence 30889, hspid=007603AI
Publication No. US2005028603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIORITY FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30880
LENGTH: 1240
TYPE: DNA
ORGANISM: Bovine
US-10-750-185-30880

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Query Match	3.3%	Score 34	DB 6	Length 1240
Best Local Similarity	46.9%	Pred. No. 2.9		
Matches 106	Conservative	0	Mismatches 120	Indels 0
			Gaps	0

Oy	125	TGCTTTTGATTTGACCAAAAGCCCATGCTGATGAATTTGACTGCGCTTCAGAACTTC	184
Db	301	TGCTTTTGCTGCTGCTAAATTTCTTCAAGTGCTGACTCTGCGCAAGCCCATAGAACTGC	360
Oy	185	AGCACAACAGGAACCTTTCCACATGGGACTGGCAATTAATAATAGCTGCTATTATAG	244
Db	361	AGCCCAACAGGCTCCCATCTACTTGTACTTCCCAAGATTAAGCTATAGCAGAA	420
Oy	245	CATCTGTGACTTTTCTTTACACTCTTCGAGGAGATTAATCCACCTTTAGCAACTTCCC	304
Db	421	CCAACTGTCCATTTTTCATGCTCTCCATTCGAAAGCACTGCTGTTTCTGAAACTTTTC	480
Oy	305	ATCAACAATTTTATTAATAATCCAACTCTGTCATCAACAAGT	350
Db	481	AATTCATCAATATTCATTTCTCAATATATTAATTCACAACACAGT	526

RESULT 7
US-10-821-234-142
; Sequence 142, Application US/10821234
; Publication No. US2005025114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit

```

?      APPLICANT:  Andartman, Susan
?      APPLICANT:  Tang, Y. Tom
?      TITLE OF INVENTION:  Methods for Diagnosis and Treatment of Preeclampsia
?      FILE REFERENCE:  821A
?      CURRENT APPLICATION NUMBER:  US/10/821,234
?      PRIOR APPLICATION NUMBER:  US 60/462,047
?      CURRENT FILING DATE:  2004-04-07
?      PRIOR FILING DATE:  2003-04-07
?      NUMBER OF SEQ ID NOS:  1704
?      SOFTWARE:  pc_seq_genes Version 1.0
?      SEQ ID NO 142
?      LENGTH:  1458
?      TYPE:  DNA
?      ORGANISM:  Homo sapiens
?      US-10-821-234-142

Query Match      3.3%;  Score 33.8;  DB 6;  Length 1458;
Best Local Similarity 47.1%;  Pred. No. 3.6;
Matches 104;  Conservative 0;  Mismatches 117;  Indels 0;  Gaps

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Query Match	3.3%;	Score	33.8;	DB	6;	Length	1458;
Best Local Similarity	47.1%;	Pred. No.	3.6;				
Matches	104;	Conservative	0;	Mismatches	117;	Indels	0;
				Gaps			0;

Qy 12 AAAGACATCAAAACCAGAAGACTTGGAAAATGAAGCCCTAGGAGAAATTAGAMGA /

Db 287 AAGACCAAATCCCATTGAAGCTGAGGCTTTGAAGCAGCTGGGTGAGAAACGAGACACGA 34

Qy 72 AGAGATTATTTGCATTAAGACACCGGAGAGACCAGCATGCTAAAGAGACCTGTGCTTT 113

Db 347 GAAAGAGTGTCTTCAGAGGCAATGAGAGACAACAACATTCACTGTAATAATGCGAGAGA 406

132 GCATTGACCAACAGCCCATGCTGATGTAATTGACTGCTCCCTCAAACTTCAGCAAC 139
 407 GAACTGACCCCAAAATGAGACTATATAAGAGAACCGAGAGGCAAAATGCTGCCAA 466

0y 192 ACAGGAACTCTTTCACAGTGGCAGTCGCCAATTAAATG 23
|||
Db 467 ACTGAACGTTCGCAGAGAAGATAAGCACTTGAAGAG 50 T

RESULT 8
US-10-750-185-48714
: Sequence 48714, Application US/10750185

```

:Publication No. US20050260603A1
:GENERAL INFORMATION:
:APPLICANT: MMT GENOMICS, INC.
:APPLICANT: DENISE, Sue K.
:APPLICANT: KERR, Richard
:APPLICANT: ROSENFELD, David
:APPLICANT: HOLM, Tom
:APPLICANT: BATES, Stephen
:APPLICANT: PANTIN, Denise
:TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
:FILE REFERENCE: MM11100-2
:CURRENT APPLICATION NUMBER: US/10/750,185
:CURRENT FILING DATE: 2003-12-31
:PRIOR APPLICATION NUMBER: US 60/437,482
:PRIOR FILING DATE: 2002-12-31
:NUMBER OF SEQ ID NOS: 64922
:SOFTWARE: PatentIn version 3.1
:SEQ ID NO 48714
:LENGTH: 2748
:TYPE: DNA
:ORGANISM: Bovine
:US-10-750-185-48714
19866880696598

```

Query Match	3.3%	Score 33.8	DB 6	Length 2748
Best Local Similarity	57.7%	Pred. No. 5		
Matches 79	Conservative 0	Mismatches 57	Indels 1	Gaps 1

Oy 789 ACTGGGCACACATTCACGCATTATTTTGGCCGGAAIAGTGGATAGATATATAAACAAII 8
 Db 666 ACTGGATAGATGACAGCATTCCTTCTTCCCTGACTCTCTATAGAGCTTAAGC-ATT 72
 Oy 849 TGTATGGTATACACCTCAACTTTTATGATAGACTTTTCCCTCCAAATGTGTCTCGAT 908

Db 725 TGATGGCAATTTGTCTACAAATTAGCATGATAGTGATGACCTAAATCTGGGGTAAAT 784
QY 909 ATTTAAAGCATACTAT 925
Db 785 TTCTAAACCAAAATCT 801

RESULT 9
US-10-750-185-38532/c
; Sequence 38532, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 38532
; LENGTH: 1840
; TYPE: DNA
; ORGANISM: Bovine 19866881352831
US-10-750-185-38532

Query Match 3.3%; Score 33.4; DB 6; Length 1840;
Best Local Similarity 58.6%; Pred. No. 5.3; Indels 0; Gaps 0;
Matches 58; Conservative 0; Mismatches 41;
QY 836 ATATAAACAATTTGTATGATATACACCTCCAACTTTTATGATAGCTTTTCCTCCAA 895
Db 1252 ATATGAAATGTATTTGCTTTGACTTATTAACCTTTTATACCTCTTTTTCAG 1193
QY 896 TTGTGTCTGATATTTAAAGCATACTATTCCTCCAT 934
Db 1192 TATCTTGTCTTAACCTTCAAGATCAGATTAAATGCAT 1154

RESULT 10
US-10-750-185-35293
; Sequence 35293, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 35293
; LENGTH: 973
; TYPE: DNA
; ORGANISM: Bovine 19866881541753
US-10-750-185-35293
Query Match 3.3%; Score 33.2; DB 6; Length 973;

Best Local Similarity 57.8%; Pred. No. 4.3;
Matches 59; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
QY 870 TTTATGATAGCTGTTTCTCCATTTGTCCTGATATTTAAAGCATACTATCT 929
Db 844 TTTTAAACGCTTGTTGCTACGCTCATAGTTTATTCAGTAAACAAGATGATACACC 903
QY 930 GCCATGCTTGAGGAGAGAACTAGTAAAGATTAGACATGTTG 971
Db 904 CCAGGCGTGAGGTGAGATCCCAAGAGAGCGCTGATG 945

RESULT 11
US-11-102-978-3/c
; Sequence 3, Application US/11102978
; Publication No. US20050250142A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Technology Transfer Office
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Diagnosis and Treatment of Herpes Simplex Virus Disease
; FILE REFERENCE: 0274-5537.1US
; CURRENT APPLICATION NUMBER: US/11/102,978
; PRIOR FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: PCT/US2003/033152
; PRIOR FILING DATE: 2003-10-18
; PRIOR APPLICATION NUMBER: 60/419,576
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 340000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (56948)..(57115)
; OTHER INFORMATION: C21orf34 exon
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (80066)..(81089)
; OTHER INFORMATION: Gene VDACP; voltage-dependent anion channel isoform 2 pseudogene
; NAME/KEY: exon
; LOCATION: (167308)..(167438)
; OTHER INFORMATION: C21orf34 exon
; FEATURE:
; NAME/KEY: exon
; LOCATION: (216732)..(216833)
; OTHER INFORMATION: C21orf34 exon
US-11-102-978-3

Query Match 3.3%; Score 33.2; DB 7; Length 340000;
Best Local Similarity 52.1%; Pred. No. 98; Indels 0; Gaps 0;
Matches 74; Conservative 0; Mismatches 68;
QY 746 AATTTCATATATTCAGAGCAAGTATGTTTCCCTTACTGGGACAAATACAG 805
Db 9668 AATTAGATATCATAGTTCAAGTACAAATTTACCTTTATTTGGCATAAAGCACA 9609
QY 806 CATGATTTTTCCTCGAATTAAGTATGATATTAACAATTTGTATGATACCTC 865
Db 9608 CAGTAGCATATTTTATTTGTCAATTTATGATTCAAAACCAAAATATATGTACCCCTT 9549
QY 866 CAACCTTTATGATAGTGTGTT 887
Db 9548 CTATGCTAAGCCAGTATAT 9527

RESULT 12
US-11-108-172-547/c
; Sequence 547, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:

```

; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secret, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongrong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 547
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-108-172-547

Query Match      3.2%; Score 32.8; DB 7; Length 399;
Best Local Similarity 55.8%; Pred. No. 3.5;
Matches 58; Conservative 2; Mismatches 44; Indels 0; Gaps 0;

QY 5 AAAGCAGAAAGACATCACAAACCAAGAAAGAACTTTGAAATGAGCCCTAGAGAAATT 64
DB 115 AAAGTAAATATGTAATATGTAATGAAATGAAAGTTTGTAAATCAACCTACGAATGA 56
QY 65 TAGAAGAGACGATTATTTGTCATAGACACGCGAGAGACCAACC 108
DB 55 TAGAACCAAGCAAGMRTYATTTAGAAAGAAACCTTTGAGACCTGC 12

RESULT 13
US-10-750-185-58068
; Sequence 58068, Application US/10750185
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
```

```

; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58068
; LENGTH: 1135
; TYPE: DNA
; ORGANISM: Bovine
; US-10-750-185-58068

Query Match      3.2%; Score 32.8; DB 6; Length 1135;
Best Local Similarity 64.5%; Pred. No. 6.1;
Matches 49; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 443 AGAAGTTCCACATTGTTGATTAAGTGAATGTTACAGAAAGCAGTTGGCTTCGA 502
DB 314 ATAACTTCACATTCATCATCAAGAGCAACAAAGAAATTTTGTGTTGTTA 373
QY 503 GTTCTTTTGTGCTGT 518
DB 374 GTTCTTTTGTGTTT 389

RESULT 14
US-10-750-185-54184
; Sequence 54184, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54184
; LENGTH: 1765
; TYPE: DNA
; ORGANISM: Bovine
; US-10-750-185-54184

Query Match      3.2%; Score 32.8; DB 6; Length 1765;
Best Local Similarity 64.5%; Pred. No. 7.8;
Matches 49; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 479 CAAGAAGCAGTTGGCTTCACATTTCTTTTGTGCTGATGATCAATTTATAGTC 538
DB 45 CAAGTAAATATTTTAAAGTTCTCATCTACTTCTTTCTGTCATGCCAAGACAGTG 104
QY 539 TGTCTTACCAATGAG 554
DB 105 TGGCCCCCTGCATAG 120

RESULT 15
US-10-986-501-27/c
; Sequence 27, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:
```

```
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 90 Human Secreted Proteins
/ FILE REFERENCE: P2013p2c1
/ CURRENT APPLICATION NUMBER: US/10/986,501
/ CURRENT FILING DATE: 2004-11-12
/ PRIOR APPLICATION NUMBER: US/10/621,363
/ PRIOR FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/969,730
/ PRIOR FILING DATE: 2001-10-06
/ PRIOR APPLICATION NUMBER: 09/774,639
/ PRIOR FILING DATE: 2001-02-01
/ PRIOR APPLICATION NUMBER: 60/238,291
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 09/244,112
/ PRIOR FILING DATE: 1999-02-04
/ PRIOR APPLICATION NUMBER: PCT/US98/16235
/ PRIOR FILING DATE: 1998-08-04
/ PRIOR APPLICATION NUMBER: 60/056,371
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,732
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,366
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,364
/ PRIOR FILING DATE: 1997-08-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 373
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 27
/ LENGTH: 1307
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-986-501-27

Query Match      3.2%; Score 32.4; DB 6; Length 1307;
Best Local Similarity 50.5%; Pred. No. 8.7;
Matches 111; Conservative 0; Mismatches 101; Indels 8; Gaps 1;

QY      590 ATCAACAGGTCCAACTAAAGAAAGATGCTGATTTGACATGATGTTGGAGAAATG 649
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      573 ATCCACAGGTGGGCAAAATGAGAGACCTCTGATGACTGATTTATTAACCA 514
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      650 AGATTATGTCGTCTGGGAATTGCGGATTGGCAATAGCTGCTGTTGGCTGTGACAT 709
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      513 AGAATGTGTCTTCTTGAACCTTTACTTCAAAACAGCTGCTTA-----GACAC 462
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      710 CTATTCATCTGTGAGTGACTTTTGACATGAGAGAAATTTCACTATATTCAAGACAAGC 769
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      461 ATATTGAACAAGTAATGCTCTTCTCTGAACAGGGTTAACGATTTTACAAACATT 402
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      770 TAGGAATTGTTCCCTTCTACTGCGCAATACAGCATT 809
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      401 AGCCCATTTTTCATCTTCTTGAAGCATCTTTTAATATT 362
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Job time : 323.456 secs

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 00:23:57 ; Search time 949.415 Seconds
(without alignments)
8858.046 Million cell updates/sec

Title: US-10-750-262-1_COPY_66_1082
Perfect score: 1017
Sequence: 1 atcgaaagcagaagacat.....ctgagatgctccagctg 1017

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodaca/1/pubpna/US08_PUBCOMB.seq: *
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4: /cgn2_6/ptodaca/1/pubpna/US10A_PUBCOMB.seq: *
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10: /cgn2_6/ptodaca/1/pubpna/US11_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1017	100.0	1177	8 US-10-696-639-15	Sequence 15, Appl
2	1017	100.0	1193	6 US-10-165-044-1	Sequence 1, Appl
3	1017	100.0	1193	7 US-10-408-009-1	Sequence 1, Appl
4	1017	100.0	1193	8 US-10-857-785-1	Sequence 1, Appl
5	1017	100.0	1193	8 US-10-856-109-1	Sequence 1, Appl
6	1017	100.0	1193	8 US-10-830-899-2	Sequence 2, Appl
7	1017	100.0	1193	8 US-10-753-195-1	Sequence 1, Appl
8	1017	100.0	1193	9 US-10-752-421-1	Sequence 1, Appl
9	1017	100.0	1193	9 US-10-861-662-2	Sequence 2, Appl
10	1017	100.0	1193	3 US-09-759-143-878	Sequence 878, App
11	1017	100.0	1193	3 US-09-780-669-878	Sequence 878, App
12	1017	100.0	1193	3 US-09-822-827-878	Sequence 878, App
13	1017	100.0	1193	3 US-09-885-793-878	Sequence 878, App
14	1017	100.0	1193	3 US-09-895-814-878	Sequence 878, App
15	1017	100.0	1193	5 US-10-012-896-878	Sequence 878, App
16	1017	100.0	1193	5 US-10-011-095-1	Sequence 1, Appl
17	1017	100.0	1193	5 US-10-010-667A-1	Sequence 1, Appl
18	1017	100.0	1193	5 US-10-205-823-396	Sequence 396, App
19	1017	100.0	1193	6 US-10-144-678A-878	Sequence 878, App
20	1017	100.0	1193	6 US-10-294-025-878	Sequence 878, App
21	1017	100.0	1193	6 US-10-393-590-35	Sequence 35, Appl
22	1017	100.0	1193	6 US-10-393-567-35	Sequence 35, Appl
23	1017	100.0	1193	6 US-10-394-087-35	Sequence 35, Appl

24	1017	100.0	1193	6 US-10-295-027-713	Sequence 713, App
25	1017	100.0	1193	6 US-10-295-027-1130	Sequence 1130, App
26	1017	100.0	1193	8 US-10-643-795A-16	Sequence 16, Appl
27	1017	100.0	1193	8 US-10-643-795A-42	Sequence 42, Appl
28	1017	100.0	1193	9 US-10-750-262-1	Sequence 1, Appl
29	1017	100.0	1193	9 US-10-948-518-16	Sequence 16, Appl
30	1017	100.0	1193	9 US-10-948-518-42	Sequence 42, Appl
31	1017	100.0	1193	9 US-10-956-157-1811	Sequence 1811, App
32	1017	100.0	1193	9 US-10-956-157-7046	Sequence 7046, App
33	1017	100.0	1193	9 US-10-858-887-1	Sequence 1, Appl
34	1017	100.0	1193	9 US-10-631-467-428	Sequence 428, App
35	1017	100.0	1193	10 US-11-051-454-396	Sequence 396, App
36	1017	100.0	1201	7 US-10-425-114-16445	Sequence 16445, A
37	1017	100.0	1277	3 US-09-814-353-19910	Sequence 19910, A
38	1017	100.0	1330	7 US-10-755-889-191	Sequence 191, App
39	988	97.1	1354	8 US-10-723-860-5120	Sequence 5120, App
40	870	85.5	1365	9 US-10-830-899-6	Sequence 6, Appl
41	870	85.5	1365	9 US-10-861-662-6	Sequence 6, Appl
42	762.2	74.9	3627	8 US-10-830-899-10	Sequence 10, Appl
43	762.2	74.9	3627	8 US-10-861-662-10	Sequence 10, Appl
44	760.6	74.8	3627	5 US-10-011-095-6	Sequence 6, Appl
45	760.6	74.8	3627	5 US-10-010-667A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-696-639-15
; Sequence 15, Application US/10696639
; Publication No. US20050037439A1
; GENERAL INFORMATION:
; APPLICANT: Bourcier, Maureen J
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; FILE REFERENCE: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; CURRENT APPLICATION NUMBER: 01040/01
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-696-639-15

Query Match 100.0%; Score 1017; DB 8; Length 1177;

Best Local Similarity 100.0%; Pred. No. 6.9e-277;

Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGAAGCAGAAAGACATCACAAACCAAGAACTTTGAAATGAAAGCTTAGAGA	60
DB	66	ATGGAAGCAGAAAGACATCACAAACCAAGAACTTTGAAATGAAAGCTTAGAGA	125
QY	61	AAATTGAAGAAGACATTTTGCATTAAGGACAGCGGAGAGCCAGCATCTAAAGA	120
DB	126	AAATTGAAGAAGACATTTTGCATTAAGGACAGCGGAGAGCCAGCATCTAAAGA	185
QY	121	CTGTGCTTTTGCATTTGCACAAAGCCATGCTGATGAATTTGACTGCCCTTGAGA	180
DB	186	CTGTGCTTTTGCATTTGCACAAAGCCATGCTGATGAATTTGACTGCCCTTGAGA	245
QY	181	CTTGAGACACACAGAACTCTTTTCAACAGTGGCACTTGGCAATTAATAGTCTGATTT	240
DB	246	CTTGAGACACACAGAACTCTTTTCAACAGTGGCACTTGGCAATTAATAGTCTGATTT	305
QY	241	ATGAGCATCTGACTTTCTTTTCACTCTTCTGAGGAAGTAATTCACCTTTAGCACT	300
DB	306	ATGAGCATCTGACTTTCTTTTCACTCTTCTGAGGAAGTAATTCACCTTTAGCACT	365

QY 301 TCCCATCAACAATATTTTAAATTCGAATCTGATCAACAAGTCTGGCAATG 360
Db 366 TCCCATCAACAATATTTTAAATTCGAATCTGATCAACAAGTCTGGCAATG 425
QY 361 GTTTCATCACTCTCTGGGATTTGTTTACCTGCAAGTGTAGAGCAATTTGCCAA 420
Db 426 GTTTCATCACTCTCTGGGATTTGTTTACCTGCAAGTGTAGAGCAATTTGCCAA 485
QY 421 CTTCAATATGAAACCAAGTATTAAGAACTTTCACATGTTGATTAAGATTTTAA 480
Db 486 CTTCAATATGAAACCAAGTATTAAGAACTTTCACATGTTGATTAAGATTTTAA 545
QY 481 AGAAGAGATTTGGGCTTCTCACTTTCTTTTGTCTGATCTGATGCAATTTATGCTG 540
Db 546 AGAAGAGATTTGGGCTTCTCACTTTCTTTTGTCTGATCTGATGCAATTTATGCTG 605
QY 541 TCTTACCATAGAGGCGATCTCTACATATAGATTAAGTGTAACTGGGATTTCAACGCTC 600
Db 606 TCTTACCATAGAGGCGATCTCTACATATAGATTAAGTGTAACTGGGATTTCAACGCTC 665
QY 601 CAACAAATTAAGAAAGATGCTGATTTGACATGATGTTGAGAAATGAGATTTATGTG 660
Db 666 CAACAAATTAAGAAAGATGCTGATTTGACATGATGTTGAGAAATGAGATTTATGTG 725
QY 661 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGTGATCTTATTCATCT 720
Db 726 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGTGATCTTATTCATCT 785
QY 721 GTGAGTGAATCTTTGACATGAGAGAAATTCATATATTCAGAGCAAGCTTAAGATTTGT 780
Db 786 GTGAGTGAATCTTTGACATGAGAGAAATTCATATATTCAGAGCAAGCTTAAGATTTGT 845
QY 781 TCCCTTCTACTGGGCAACAATACAGCATGATTTTGGCTGGAATTAAGATTAAGATTA 840
Db 846 TCCCTTCTACTGGGCAACAATACAGCATGATTTTGGCTGGAATTAAGATTAAGATTA 905
QY 841 AACAATTTGTATGATGATTAACCTCCCACTTTATGATAGCTGTTTCTTCCATTTGT 900
Db 906 AACAATTTGTATGATGATTAACCTCCCACTTTATGATAGCTGTTTCTTCCATTTGT 965
QY 901 GTCCATATTTTAAAGCATACTATTCCTGCGATGCTGGAAGAAATGATGAGATTT 960
Db 966 GTCCATATTTTAAAGCATACTATTCCTGCGATGCTGGAAGAAATGATGAGATTT 1025
QY 961 AGACATGTTGGGAGACGTCAACCAAAATTAACAAAATGAGATTTGTTCCAGTTG 1017
Db 1026 AGACATGTTGGGAGACGTCAACCAAAATTAACAAAATGAGATTTGTTCCAGTTG 1082

RESULT 2
US-10-165-044-1
; Sequence 1, Application US/10165044
; Publication No. US20030149531A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas Saffran
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Steven Chappell Mitchell
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; FILE REFERENCE: 51158-20016.02
; CURRENT APPLICATION NUMBER: US/10/165,044
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01

; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: WO 99/62941
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/US00/33040
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1191)
US-10-165-044-1

Query Match 100.0%; Score 1017; DB 6; Length 1193;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAAGAGAGAAAGATCAACAACCAAGAAACCTTGGAAATGAAGCTTAGAGACA 60
Db 64 ATGGAAGAGAGAAAGATCAACAACCAAGAAACCTTGGAAATGAAGCTTAGAGACA 123
QY 61 AATTGGAAGAGACGATTAATTTGATTAAGACACGGGAGAGACAGCATGCTTAAAGAA 120
Db 124 AATTGGAAGAGACGATTAATTTGATTAAGACACGGGAGAGACAGCATGCTTAAAGAA 183
QY 121 CCTGTCTTTTGCATTTGACCAACACGCCATGCTGATGAATTTGATGCTGCTTCAAG 180
Db 184 CCTGTCTTTTGCATTTGACCAACACGCCATGCTGATGAATTTGATGCTGCTTCAAG 243
QY 181 CTTGAGCACACAGAGAACTTTTCCAGAGTGGCACTTSCCAATTAATTAAGTCTGAT 240
Db 244 CTTGAGCACACAGAGAACTTTTCCAGAGTGGCACTTSCCAATTAATTAAGTCTGAT 303
QY 241 ATAGCATCTGACATTTTCTTACACTCTTCTGAGGGAATTAATCACCCCTTAGCACT 300
Db 304 ATAGCATCTGACATTTTCTTACACTCTTCTGAGGGAATTAATCACCCCTTAGCACT 363
QY 301 TCCCATCAACAATATTTTAAATTCGAATCTGCTGATCAACAAGTCTTGGCAATG 360
Db 364 TCCCATCAACAATATTTTAAATTCGAATCTGCTGATCAACAAGTCTTGGCAATG 423
QY 361 GTTTCATCACTCTGTTGGCATTTGTTTACCTGCGAGGATGATGAGCAATTTGCCAA 420
Db 424 GTTTCATCACTCTGTTGGCATTTGTTTACCTGCGAGGATGATGAGCAATTTGCCAA 483
QY 421 CTTCAATATGAAACCAAGTATTAAGAACTTTCACATGTTGATTAAGATTTTAA 480
Db 484 CTTCAATATGAAACCAAGTATTAAGAACTTTCACATGTTGATTAAGATTTTAA 543
QY 481 AGAAGAGATTTGGGCTTCTCACTTTCTTTTGTCTGATCTGATGCAATTTATGCTG 540
Db 544 AGAAGAGATTTGGGCTTCTCACTTTCTTTTGTCTGATCTGATGCAATTTATGCTG 603
QY 541 TCTTACCATAGAGGCGATCTCTACATATAGATTAAGTGTAACTGGGATTTCAACGCTC 600
Db 604 TCTTACCATAGAGGCGATCTCTACATATAGATTAAGTGTAACTGGGATTTCAACGCTC 663
QY 601 CAACAAATTAAGAAAGATGCTGATTTGAGATGATTTTGGAGATGAGATTTATGTG 660
Db 664 CAACAAATTAAGAAAGATGCTGATTTGAGATGATTTTGGAGATGAGATTTATGTG 723
QY 661 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGTGATCTTATTCATCT 720
Db 724 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGTGATCTTATTCATCT 783
QY 721 GTGAGTGAATCTTTGACATGAGAGAAATTCATATATTCAGAGCAAGCTTAAGATTTGT 780
Db 784 GTGAGTGAATCTTTGACATGAGAGAAATTCATATATTCAGAGCAAGCTTAAGATTTGT 843

Qy 781 TCCCTTCTACTGGGCAACAATACGCAATGATTTTGGCTGGAAATTAAGTAGATATATA 840
Db 844 TCCCTTCTACTGGGCAACAATACGCAATGATTTTGGCTGGAAATTAAGTAGATATATA 903
Qy 841 AAACAAATTTGATGTATACACCTTCCAACTTTTATGATAGCTTTTCTTCCAAATGTT 900
Db 904 AAACAAATTTGATGTATACACCTTCCAACTTTTATGATAGCTTTTCTTCCAAATGTT 963
Qy 901 GTCCGATATTTTAAAGCACTATCTTCCGCAATGCTTGAAGAGAAATATCTGAAGATT 960
Db 964 GTCCGATATTTTAAAGCACTATCTTCCGCAATGCTTGAAGAGAAATATCTGAAGATT 1023
Qy 961 AGACATGTTGGGAAGACGTCAACCAAAATTAACAACTGATATGTTCCAGTTG 1017
Db 1024 AGACATGTTGGGAAGACGTCAACCAAAATTAACAACTGATATGTTCCAGTTG 1080

RESULT 3

US-10-408-009-1
; Sequence 1, Application US/10408009
; Publication No. US20040072196A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; FILE REFERENCE: 511582001603
; CURRENT APPLICATION NUMBER: US/10/408, 009
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)
US-10-408-009-1

Query Match 100.0%; Score 1017; DB 7; Length 1193;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAAGAGCAAAAGACATCAACCAAGAAAGACTTTGGAAAATGAAGCCCTAGAGAGA 60
Db 64 ATGGAAGAGCAAAAGACATCAACCAAGAAAGACTTTGGAAAATGAAGCCCTAGAGAGA 123
Qy 61 AATTAGAAGAGCAATTTATTTGATTAAGAGACGAGGAGACAGAGATCTTAAAGA 120
Db 124 AATTAGAAGAGCAATTTATTTGATTAAGAGACGAGGAGACAGAGATCTTAAAGA 183
Qy 121 CTTGTGCTTTTGGATTTGACCAAAAGCCCATCTGATGAATTTGACTGCCCTTCAGAA 180
Db 184 CTTGTGCTTTTGGATTTGACCAAAAGCCCATCTGATGAATTTGACTGCCCTTCAGAA 243
Qy 181 CTTAGACACACAGGAACCTTTTCCAGAGTGGCACTTGGCAATTTAAATAGCTGATTT 240
Db 244 CTTAGACACACAGGAACCTTTTCCAGAGTGGCACTTGGCAATTTAAATAGCTGATTT 303
Qy 241 ATAGCATCTGACATTTTCTTACACCTTTCTGAGGGAAGTAATTCACCCCTTAGCAACT 300
Db 304 ATAGCATCTGACATTTTCTTACACCTTTCTGAGGGAAGTAATTCACCCCTTAGCAACT 363
Qy 301 TCCCATCAACAATATTTTATTAATAATTCATCTGTGTCATCAACAAAGTCTTCCAAATG 360

Db 364 TCCCATCAACAATATTTTATTAATAATTCATCTGTGTCATCAACAAAGTCTTCCAAATG 423
Qy 361 GTTTCATCACTCTTGGCAATGTTTACCTGCGCAGGTGTAGAGCAAAATGTCCAA 420
Db 424 GTTTCATCACTCTTGGCAATGTTTACCTGCGCAGGTGTAGAGCAAAATGTCCAA 483
Qy 421 CTTGATATGGAACCAAGTATTAAGAAATTTCCAACTTTGTTGATTAAGTATTAACA 480
Db 484 CTTGATATGGAACCAAGTATTAAGAAATTTCCAACTTTGTTGATTAAGTATTAACA 543
Qy 481 AGAAGAGATTTGGGCTTCTCAAGTTTCTTTTGGTGTACTGATGCAATTTATAGCTG 540
Db 544 AGAAGAGATTTGGGCTTCTCAAGTTTCTTTTGGTGTACTGATGCAATTTATAGCTG 603
Qy 541 TCTTACCAATGAGGCGATCTCTACAGTACAGTGTCTAACTGGGCAATCAACAGGTC 600
Db 604 TCTTACCAATGAGGCGATCTCTACAGTACAGTGTCTAACTGGGCAATCAACAGGTC 663
Qy 601 CAACAAATTAAGAGATGCTGTGATGACATGATGTTGGAGATGAGATTTATGTG 660
Db 664 CAACAAATTAAGAGATGCTGTGATGACATGATGTTGGAGATGAGATTTATGTG 723
Qy 661 TCTGTGGAAATTTGGGATTTGGCAATTCCTGCTCTGTGGCTGTGACATCTATTCATCT 720
Db 724 TCTGTGGAAATTTGGGATTTGGCAATTCCTGCTCTGTGGCTGTGACATCTATTCATCT 783
Qy 721 GTGAGTACCTTTGACATGAGAGAAATTCACATATTTAGAGCAAGCTTAGGAATGTT 780
Db 784 GTGAGTACCTTTGACATGAGAGAAATTCACATATTTAGAGCAAGCTTAGGAATGTT 843
Qy 781 TCCCTTCTACTGGGCAACAATACGCAATGATTTTGGCTGGAAATTAAGTAGATATATA 840
Db 844 TCCCTTCTACTGGGCAACAATACGCAATGATTTTGGCTGGAAATTAAGTAGATATATA 903
Qy 841 AAACAAATTTGATGTATACACCTTCCAACTTTTATGATAGCTTTTCTTCCAAATGTT 900
Db 904 AAACAAATTTGATGTATACACCTTCCAACTTTTATGATAGCTTTTCTTCCAAATGTT 963
Qy 901 GTCCGATATTTTAAAGCACTATCTTCCGCAATGCTTGAAGAGAAATATCTGAAGATT 960
Db 964 GTCCGATATTTTAAAGCACTATCTTCCGCAATGCTTGAAGAGAAATATCTGAAGATT 1023
Qy 961 AGACATGTTGGGAAGACGTCAACCAAAATTAACAACTGATATGTTCCAGTTG 1017
Db 1024 AGACATGTTGGGAAGACGTCAACCAAAATTAACAACTGATATGTTCCAGTTG 1080

RESULT 4

US-10-857-785-1
; Sequence 1, Application US/10857785
; Publication No. US20040219162A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; FILE REFERENCE: 511582001607
; CURRENT APPLICATION NUMBER: US/10/857,785
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1

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; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)
US-10-857-785-1
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Query Match      100.0%; Score 1017; DB 8; Length 1193;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGGAAGAGAGAAAGACATCAACCAAGAACTTTGGAAATGAACCTTAGAGA 60
DB 64 ATGGAAGAGAGAAAGACATCAACCAAGAACTTTGGAAATGAACCTTAGAGA 123
QY 61 AATTGGAAGAGAGAAAGACATCAACCAAGAACTTTGGAAATGAACCTTAGAGA 120
DB 124 AATTGGAAGAGAGAAAGACATCAACCAAGAACTTTGGAAATGAACCTTAGAGA 183
QY 121 CTTGCTGCTTTGGATTTGGACACCAAGCCCATGCTGATGAATTTGACCTCCCTAGAA 180
DB 184 CTTGCTGCTTTGGATTTGGACACCAAGCCCATGCTGATGAATTTGACCTCCCTAGAA 243
QY 181 CTTGAGACACACAGAGAACTCTTTCCACAGTGGCACTTGCCTAATTAATAGCTGCTATT 240
DB 244 CTTGAGACACACAGAGAACTCTTTCCACAGTGGCACTTGCCTAATTAATAGCTGCTATT 303
QY 241 ATAGCATCTGCTCTTTCTTTACACTCTTTGAGGAACTAATTCACCTTTAGCAACT 300
DB 304 ATAGCATCTGCTCTTTCTTTACACTCTTTGAGGAACTAATTCACCTTTAGCAACT 363
QY 301 TCCCATCAACAATATTTTATTAATAATTCATCTGCTGCTCAACAAGCTTTGCCAATG 360
DB 364 TCCCATCAACAATATTTTATTAATAATTCATCTGCTGCTCAACAAGCTTTGCCAATG 423
QY 361 GTTTTCATCACTCTCTTTGCACTGTTTACCTGCGACAGTGTATAGCAGCAATTTGCCAA 420
DB 424 GTTTTCATCACTCTCTTTGCACTGTTTACCTGCGACAGTGTATAGCAGCAATTTGCCAA 483
QY 421 CTTCAATATGGAACCAAGTATTAAGAACTTCCACATGTTGTAATAGTGAATGTTAAACA 480
DB 484 CTTCAATATGGAACCAAGTATTAAGAACTTCCACATGTTGTAATAGTGAATGTTAAACA 543
QY 481 AGAAGAGAGTTGGGCTTCTCACTTTCTTTTGTCTGTAATGCAATGCAATTTAGCTG 540
DB 544 AGAAGAGAGTTGGGCTTCTCACTTTCTTTTGTCTGTAATGCAATGCAATTTAGCTG 603
QY 541 TCTTACCCAAATGAGGCGATCTTAACATACAGTGTCTAACTGGGCAATCAACAGGTC 600
DB 604 TCTTACCCAAATGAGGCGATCTTAACATACAGTGTCTAACTGGGCAATCAACAGGTC 663
QY 601 CAACAAATTAAGAAGATGCTGATGAGCAATGAGTGTGGAATGGAATTTATGAGT 660
DB 664 CAACAAATTAAGAAGATGCTGATGAGCAATGAGTGTGGAATGGAATTTATGAGT 723
QY 661 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGCTGTAATCTATTTCCATCT 720
DB 724 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGCTGTAATCTATTTCCATCT 783
QY 721 GTGAGTGAATCTTTGACATGAGAGAAATTTCACTAATTCAGAGCAAGCTTAGGAATTTGTT 780
DB 784 GTGAGTGAATCTTTGACATGAGAGAAATTTCACTAATTCAGAGCAAGCTTAGGAATTTGTT 843
QY 781 TCCCTTCTACTGGGCAACAATACAGCATTAATTTTGGCTGGAAATAGTGAATTAATTA 840
DB 844 TCCCTTCTACTGGGCAACAATACAGCATTAATTTTGGCTGGAAATAGTGAATTAATTA 903
QY 841 AAACAATTTGTATGATATACCTCAACTTTTATGATAGCTGTTTCTTCCCAATTTGTT 900
DB 904 AAACAATTTGTATGATATACCTCAACTTTTATGATAGCTGTTTCTTCCCAATTTGTT 963
QY 901 GTCTGATATTTTAAAGCATACTAATTCCTGCAATGCTTGAAGAAAGATTAAGAAATTT 960
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DB 964 GTCTGATATTTTAAAGCATACTAATTCCTGCAATGCTTGAAGAAAGATTAAGAAATTT 1023
QY 961 AGACATGTTGGGAAGAGCTGCACCAAAATTAACAAACTGAGATATGTTCCAGTTG 1017
DB 1024 AGACATGTTGGGAAGAGCTGCACCAAAATTAACAAACTGAGATATGTTCCAGTTG 1080
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RESULT 5
US-10-856-109-1
; Sequence 1, Application US/10856109
; Publication No. US20040219591A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; FILE REFERENCE: 511582001606
; CURRENT APPLICATION NUMBER: US/10/856,109
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)
US-10-856-109-1
```

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Query Match      100.0%; Score 1017; DB 8; Length 1193;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 ATGGAAGAGAGAAAGACATCAACCAAGAACTTTGGAAATGAACCTTAGAGA 60
DB 64 ATGGAAGAGAGAAAGACATCAACCAAGAACTTTGGAAATGAACCTTAGAGA 123
QY 61 AATTGGAAGAGAGAAAGACATCAACCAAGAACTTTGGAAATGAACCTTAGAGA 120
DB 124 AATTGGAAGAGAGAAAGACATCAACCAAGAACTTTGGAAATGAACCTTAGAGA 183
QY 121 CTTGCTGCTTTGGATTTGGACACCAAGCCCATGCTGATGAATTTGACCTCCCTAGAA 180
DB 184 CTTGCTGCTTTGGATTTGGACACCAAGCCCATGCTGATGAATTTGACCTCCCTAGAA 243
QY 181 CTTGAGACACACAGAGAACTCTTTCCACAGTGGCACTTGCCTAATTAATAGCTGCTATT 240
DB 244 CTTGAGACACACAGAGAACTCTTTCCACAGTGGCACTTGCCTAATTAATAGCTGCTATT 303
QY 241 ATAGCATCTGCTCTTTCTTTACACTCTTTGAGGAACTAATTCACCTTTAGCAACT 300
DB 304 ATAGCATCTGCTCTTTCTTTACACTCTTTGAGGAACTAATTCACCTTTAGCAACT 363
QY 301 TCCCATCAACAATATTTTATTAATAATTCATCTGCTGCTGATCAACAAGCTTTGCCAATG 360
DB 364 TCCCATCAACAATATTTTATTAATAATTCATCTGCTGCTGATCAACAAGCTTTGCCAATG 423
QY 361 GTTTTCATCACTCTCTTTGCACTGTTTACCTGCGACAGTGTATAGCAGCAATTTGCCAA 420
DB 424 GTTTTCATCACTCTCTTTGCACTGTTTACCTGCGACAGTGTATAGCAGCAATTTGCCAA 483
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QY 421 CTTGATATGGAACCAAGTATTAAGAGTTTCCACATGTTGATTAAGTGAATGTTAACA 480
DB 484 CTTGATATGGAACCAAGTATTAAGAGTTTCCACATGTTGATTAAGTGAATGTTAACA 543
QY 481 AGAAGCAGTTGGGCTTCTCAGTTCTTTTCTGTAAGTGAATTAAGTCTG 540
DB 544 AGAAGCAGTTGGGCTTCTCAGTTCTTTTCTGTAAGTGAATTAAGTCTG 603
QY 541 TCTTACCAATGAGGCAATCTTACAGATTAAGTGAATTAAGTGAATTAAGTCTG 600
DB 604 TCTTACCAATGAGGCAATCTTACAGATTAAGTGAATTAAGTGAATTAAGTCTG 663
QY 601 CAACAAATTAAGAGAGTGGCTGATTAAGTGAATTAAGTGAATTAAGTCTG 660
DB 664 CAACAAATTAAGAGAGTGGCTGATTAAGTGAATTAAGTGAATTAAGTCTG 723
QY 661 TCTTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGATTAAGTCTG 720
DB 724 TCTTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGATTAAGTCTG 783
QY 721 GTAGAGCTCTTGAATGAGAGATTAAGTGAATTAAGTGAATTAAGTCTG 780
DB 784 GTAGAGCTCTTGAATGAGAGATTAAGTGAATTAAGTGAATTAAGTCTG 843
QY 781 TCCCTTCTAGTGGCAATACAGCATGATTTTCTGAAATTAAGTGAATTAAGTCTG 840
DB 844 TCCCTTCTAGTGGCAATACAGCATGATTTTCTGAAATTAAGTGAATTAAGTCTG 903
QY 841 AAACAAATTTGATGATACACCTCCAACTTTTATGATGATTTTCTTCCAAATGTT 900
DB 904 AAACAAATTTGATGATACACCTCCAACTTTTATGATGATTTTCTTCCAAATGTT 963
QY 901 GTCTGATATTTAAAGCATATTTCTGCAATGCTTGAAGAGAGATTAAGTCTG 960
DB 964 GTCTGATATTTAAAGCATATTTCTGCAATGCTTGAAGAGAGATTAAGTCTG 1023
QY 961 AGACATGTTGGGAGAGCTCACCAAAATTAAGAGATTAAGTCTG 1017
DB 1024 AGACATGTTGGGAGAGCTCACCAAAATTAAGAGATTAAGTCTG 1080

RESULT 6
US-10-830-899-2
; Sequence 2, Application US/10830899
; Publication No. US20040253232A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Etesami, Soudabeh
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Perez-Villar, Juan
; APPLICANT: Meyrick Morrison, Karen Jane
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Faris, Mary
; APPLICANT: Guadas, Jean
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: Antibodies and Molecules Derived
; TITLE OF INVENTION: therefrom that Bind to STEAP-1 Proteins
; FILE REFERENCE: 51158-20016.26
; CURRENT APPLICATION NUMBER: US/10/830,899
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 10/010,667
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 10/011,095
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 10/236,878
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
```

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; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66) ... (1085)
US-10-830-899-2

Query Match 100.0%; Score 1017; DB 8; Length 1193;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAAGCAGAAACATCAACAAACCAAGAACTTTGGAATTAAGTGAATGAGTGA 60
DB 66 ATGGAAGCAGAAACATCAACAAACCAAGAACTTTGGAATTAAGTGAATGAGTGA 125
QY 61 AATTGAAGAGACATTAATTGATTAAGAGACCGGAGAGACAGCATGCTTAAAGA 120
DB 126 AATTGAAGAGACATTAATTGATTAAGAGACCGGAGAGACAGCATGCTTAAAGA 185
QY 121 CTTGCTCTTTGATTTGCAACCAAGCCCATGCTGATGAATTTGACTGCTTCAAG 180
DB 186 CTTGCTCTTTGATTTGCAACCAAGCCCATGCTGATGAATTTGACTGCTTCAAG 245
QY 181 CTTGACACACACAGAGACCTTTTCCAGAGTGGCACTTTGCAATTAAGTGAAT 240
DB 246 CTTGACACACACAGAGACCTTTTCCAGAGTGGCACTTTGCAATTAAGTGAAT 305
QY 241 ATAGCATCTGACTCTTTCTTTACACTCTTTCTGAGGAGATTAATCACTTGAAG 300
DB 306 ATAGCATCTGACTCTTTCTTTACACTCTTTCTGAGGAGATTAATCACTTGAAG 365
QY 301 TCCCATCAACATATTTTATTAATAATTCATCTGCTGATCAACAAAGCTTTGCCA 360
DB 366 TCCCATCAACATATTTTATTAATAATTCATCTGCTGATCAACAAAGCTTTGCCA 425
QY 361 GTTTCATCACTCTCTTGGCATTTGTTTACCTGCGAGGTGTATACAGCAATTTGCC 420
DB 426 GTTTCATCACTCTCTTGGCATTTGTTTACCTGCGAGGTGTATACAGCAATTTGCC 485
QY 421 CTTGATATGGAACCAAGTATTAAGAGTTTCCACATGTTGATTAAGTGAATGTTAACA 480
DB 486 CTTGATATGGAACCAAGTATTAAGAGTTTCCACATGTTGATTAAGTGAATGTTAACA 545
QY 481 AGAAGCAGTTGGGCTTCTCAGTTCTTTTCTGTAAGTGAATTAAGTCTG 540
DB 546 AGAAGCAGTTGGGCTTCTCAGTTCTTTTCTGTAAGTGAATTAAGTCTG 605
QY 541 TCTTACCAATGAGGAGATCTTACAGATTAAGTGAATTAAGTGAATTAAGTCTG 600
DB 606 TCTTACCAATGAGGAGATCTTACAGATTAAGTGAATTAAGTGAATTAAGTCTG 665
QY 601 CAACAAATTAAGAGAGTGGCTGATTAAGTGAATTAAGTGAATTAAGTCTG 660
DB 666 CAACAAATTAAGAGAGTGGCTGATTAAGTGAATTAAGTGAATTAAGTCTG 725
QY 661 TCTTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGATTAAGTCTG 720
DB 726 TCTTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGATTAAGTCTG 785
QY 721 GTAGAGCTCTTGAATGAGAGATTAAGTGAATTAAGTGAATTAAGTCTG 780
DB 786 GTAGAGCTCTTGAATGAGAGATTAAGTGAATTAAGTGAATTAAGTCTG 845
QY 781 TCCCTTCTAGTGGCAATACAGCATGATTTTCTGAAATTAAGTGAATTAAGTCTG 840
DB 846 TCCCTTCTAGTGGCAATACAGCATGATTTTCTGAAATTAAGTGAATTAAGTCTG 905
QY 841 AAACAAATTTGATGATACACCTCCAACTTTTATGATGATTTTCTTCCAAATGTT 900
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Db 906 AACCAATTTGTAAGTATACCTCCAACTTTTATGATAGCTGTTTCTTCCATTTGTT 965
QY 901 GTCTGATATTTAAAGCATACTATTCCTGCATGCTTGAGAGAAAGATCTGAAGATT 960
Db 966 GTCCGATATTTAAAGATATACTATTCCTGCATGCTTGAGAGAAAGATCTGAAGATT 1025
QY 961 AGACATGTTGGGAAGAGCTCACCAAATTTAACAAACCTGAGATATGTTTCCAGTTG 1017
Db 1026 AGACATGTTGGGAAGAGCTCACCAAATTTAACAAACCTGAGATATGTTTCCAGTTG 1082

RESULT 7

US-10-753-195-1
; Sequence 1, Application US/10753195
; Publication No. US2005004349A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas Saffran
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Steven Chappel Mitchell
; APPLICANT: Mary Farris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 51158-20016.02
; CURRENT APPLICATION NUMBER: US/10/753,195
; PRIOR FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: US/60/165,044
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: WO 99/62941
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/US00/33040
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64) ... (1191)
US-10-753-195-1

Query Match 100.0%; Score 1017; DB 8; Length 1193;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAAGAGAGAAAGACATCACAAAACCAAGAACTTTGAAAAATGAAGCTTAGAGAG 60
Db 64 ATGGAAGAGAGAAAGACATCACAAAACCAAGAACTTTGAAAAATGAAGCTTAGAGAG 123
QY 61 AATTGAGAAGAGACGATTATTTGCAATTAAGACACGGAGAGACACGATGCTTAAAAAG 120
Db 124 AATTGAGAAGAGACGATTATTTGCAATTAAGACACGGAGAGACACGATGCTTAAAAAG 183
QY 121 CCTGTCCTTTTGCAATTTGACCAAAACGCCCATGCTGATGAATTTGACTGCCCTTGAGAA 180
Db 184 CCTGTCCTTTTGCAATTTGACCAAAACGCCCATGCTGATGAATTTGACTGCCCTTGAGAA 243
QY 181 CTTGACACACACAGGAACCTTTCCACAGTGGCACTTGGCAATTTAAATAGCTGCTATT 240
Db 244 CTTGACACACACAGGAACCTTTCCACAGTGGCACTTGGCAATTTAAATAGCTGCTATT 303

QY 241 ATAGCATCTGACTTTTCTTACACTCTTCTGAGGGAGATTAACCCCTTAGCAACT 300
Db 304 ATAGCATCTGACTTTTCTTACACTCTTCTGAGGGAGATTAACCCCTTAGCAACT 363
QY 301 TCCATCAACAATATTTTATTAATTAATTCATCTCTGTCATCAACAAAGCTTCCCAATG 360
Db 364 TCCATCAACAATATTTTATTAATTAATTCATCTCTGTCATCAACAAAGCTTCCCAATG 423
QY 361 GTTTCATCACTCTCTTGGCATTTGTTTACTGTCAGAGTGTGATAGCAAGAAATGTCCAA 420
Db 424 GTTTCATCACTCTCTTGGCATTTGTTTACTGTCAGAGTGTGATAGCAAGAAATGTCCAA 483
QY 421 CTTCAATAATGAAACAGTAAAGATTTTCCATTTGTTGATGTTGAATGATGATTAACA 480
Db 484 CTTCAATAATGAAACAGTAAAGATTTTCCATTTGTTGATGTTGAATGATGATTAACA 543
QY 481 AGAAGCAGTTGGGCTTCTCAGTTTCTTTTGTCTGACTGATGCAATTTATAGTGTG 540
Db 544 AGAAGCAGTTGGGCTTCTCAGTTTCTTTTGTCTGACTGATGCAATTTATAGTGTG 603
QY 541 TCTTACCAATGAGGCGATCTTCAAGATCAAGTTGCTTAACTGGGCAATTCACAGGTG 600
Db 604 TCTTACCAATGAGGCGATCTTCAAGATCAAGTTGCTTAACTGGGCAATTCACAGGTG 663
QY 601 CAACAATAATTAAGAGATGCTGATGAGATGATGTTGAGATGAGATTTATGTG 660
Db 664 CAACAATAATTAAGAGATGCTGATGAGATGATGTTGAGATGAGATTTATGTG 723
QY 661 TCTGAGGAATTTGAGATTTGGCAATACCTGCTCTGTTGAGTGTGATCTATTTCATCT 720
Db 724 TCTGAGGAATTTGAGATTTGGCAATACCTGCTCTGTTGAGTGTGATCTATTTCATCT 783
QY 721 GTGAGTGACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAACCTGGAATGTT 780
Db 784 GTGAGTGACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAACCTGGAATGTT 843
QY 781 TCCCTTCACTGGGAGCAATACGCAATTTTGGCTGGAATTAAGTGAATGATATA 840
Db 844 TCCCTTCACTGGGAGCAATACGCAATTTTGGCTGGAATTAAGTGAATGATATA 903
QY 841 AAACAATTTGATGATATACCTTCCAACTTTTATGATAGCTGTTTCCCAATGTT 900
Db 904 AAACAATTTGATGATATACCTTCCAACTTTTATGATAGCTGTTTCCCAATGTT 963
QY 901 GTCTGATATTTAAAGCATACTATTCCTGCATGCTTGAGAGAAAGATCTGAAGATT 960
Db 964 GTCTGATATTTAAAGCATACTATTCCTGCATGCTTGAGAGAAAGATCTGAAGATT 1023
QY 961 AGACATGTTGGGAAGAGCTCACCAAATTTAACAAACCTGAGATATGTTTCCAGTTG 1017
Db 1024 AGACATGTTGGGAAGAGCTCACCAAATTTAACAAACCTGAGATATGTTTCCAGTTG 1080

RESULT 8

US-10-752-421-1
; Sequence 1, Application US/10752421
; Publication No. US20050063975A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 511582001612
; CURRENT APPLICATION NUMBER: US/10/752,421
; PRIOR FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01

PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FaSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1193
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (64)...(1083)
US-10-752-421-1

Query Match 100.0%; Score 1017; DB 9; Length 1193;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGAAGCAGAAAGCATCACAAACAGAAAGAACTTTGAAATGAAAGCTAGAGAGA 60
64 ATGGAAGCAGAAAGCATCACAAACAGAAAGAACTTTGAAATGAAAGCTAGAGAGA 123
61 AATTGAGAAGAGCGATTATTGATAGAGACACGGAGAGACACAGCATGCTAAAAAGA 120
124 AATTGAGAAGAGCGATTATTGATAGAGACACGGAGAGACACAGCATGCTAAAAAGA 183
121 CCGTGCTTTTGATTTGGACCAAAAGCCCATGCTGATGAAATTTGACCTGCTTGAGA 180
184 CCGTGCTTTTGATTTGGACCAAAAGCCCATGCTGATGAAATTTGACCTGCTTGAGA 243
181 CTTGACACACACAGAACTCTTCCACAGTGGCACTTGGCAATTAATAGCTGCTATT 240
244 CTTGACACACACAGAACTCTTCCACAGTGGCACTTGGCAATTAATAGCTGCTATT 303
241 ATAGCATCTGACTTTCTTTTACACTCTTCTGAGGAGAAATTCACCTTTAGCAACT 300
304 ATAGCATCTGACTTTCTTTTACACTCTTCTGAGGAGAAATTCACCTTTAGCAACT 363
301 TCCCATCAACAATTTTAAATTTTAAATTCCTGCTGCTCAACAAAGCTTGGCAAGT 360
364 TCCCATCAACAATTTTAAATTTTAAATTCCTGCTGCTCAACAAAGCTTGGCAAGT 423
361 GTTTCATCACTCTTCTGCACTGTTTACCTCCAGAGTGTGATAGAGAAATTTGCCAA 420
424 GTTTCATCACTCTTCTGCACTGTTTACCTCCAGAGTGTGATAGAGAAATTTGCCAA 483
421 CTTCATATATGAAACCAAGTATGAAGAGTTTCCACATTTGTTGATTAAGTATTAACA 480
484 CTTCATATATGAAACCAAGTATGAAGAGTTTCCACATTTGTTGATTAAGTATTAACA 543
481 AGAAAGCAATTTGGGCTTCTCACTTTTCTTTTGGCTGATGATGCAATTTATAGTCTG 540
544 AGAAAGCAATTTGGGCTTCTCACTTTTCTTTTGGCTGATGATGCAATTTATAGTCTG 603
541 TCTTACCAATGAGGCGATCTCTACAGATCAAGTTGCTAACTGGGCAATATCAACAGGTC 600
604 TCTTACCAATGAGGCGATCTCTACAGATCAAGTTGCTAACTGGGCAATATCAACAGGTC 663
601 CAACAAATTAAGAAAGATGCTGATGATGATGATGATGATGATGATGATGATGATG 660
664 CAACAAATTAAGAAAGATGCTGATGATGATGATGATGATGATGATGATGATGATG 723
661 TCTTGGGAAATTTGGGATTTGGCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
724 TCTTGGGAAATTTGGGATTTGGCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783
721 GTGAGTGAATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
784 GTGAGTGAATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 843
781 TCCCTTCTACTGGGCAATTAACAGCATTTGTTGCTGGAATTAAGTATGATATATA 840

844 TCCCTTCTACTGGGCAATTAACAGCATTTGTTGCTGGAATTAAGTATGATATATA 903
841 AACCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
904 AACCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 963
901 GTCCGATATTTTAAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 960
964 GTCCGATATTTTAAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1023
961 AGACATGTTGGGAGAGCGTACCAAAATTAACAAATGATGATGATGATGATGATGATG 1017
1024 AGACATGTTGGGAGAGCGTACCAAAATTAACAAATGATGATGATGATGATGATGATG 1080

RESULT 9
US-10-861-662-2
Sequence 2, Application US/10861662
Publication No. US20050086707A1
GENERAL INFORMATION:

APPLICANT: Jakobovits, Aya
APPLICANT: Etesami, Soudabeh
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Perez-Villar, Juan
APPLICANT: Meyrick Morrison, Karen Jane
APPLICANT: Jia, Xiao-Chi
APPLICANT: Faris, Mary
APPLICANT: Gudae, Jean
APPLICANT: Raitano, Arthur B.
TITLE OF INVENTION: Antibodies and Molecules Derived
FILE REFERENCE: 51158-20016.26
CURRENT APPLICATION NUMBER: US/10/861,662
PRIOR FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 10/010,667
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 10/011,095
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 10/236,878
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 103
SOFTWARE: FaSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1193
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (66)...(1085)
US-10-861-662-2

Query Match 100.0%; Score 1017; DB 9; Length 1193;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGAAGCAGAAAGCATCACAAACAGAAAGAACTTTGAAATGAAAGCTAGAGAGA 60
66 ATGGAAGCAGAAAGCATCACAAACAGAAAGAACTTTGAAATGAAAGCTAGAGAGA 125
61 AATTGAGAAGAGCGATTATTGATAGAGACACGGAGAGACACAGCATGCTAAAAAGA 120
126 AATTGAGAAGAGCGATTATTGATAGAGACACGGAGAGACACAGCATGCTAAAAAGA 185
121 CCGTGCTTTTGATTTGGACCAAAAGCCCATGCTGATGAAATTTGACCTGCTTGAGA 180
186 CCGTGCTTTTGATTTGGACCAAAAGCCCATGCTGATGAAATTTGACCTGCTTGAGA 245

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OY 181 CTTGACGACACAGAACTCTTTCACAGTGGCACTTGCATTTAAATAGCTGCTATT 240
Db 246 CTTGACGACACAGAACTCTTTCACAGTGGCACTTGCATTTAAATAGCTGCTATT 305
OY 241 ATAGCATCTGACTTTTCTTTTACCTCTTCTGAGGGAAGTATTCACCTTTAGCACT 300
Db 306 ATAGCATCTGACTTTTCTTTTACCTCTTCTGAGGGAAGTATTCACCTTTAGCACT 365
OY 301 TCCCATCAACAATATTTTAAATTCGAATCTGTGCATCAACAAGTCTGGCAATG 360
Db 366 TCCCATCAACAATATTTTAAATTCGAATCTGTGCATCAACAAGTCTGGCAATG 425
OY 361 GTTTCATCACTCTCTTGGCACTTGGTTTAACTGCGAGGTGTAGAGCAATTTGCCA 420
Db 426 GTTTCATCACTCTCTTGGCACTTGGTTTAACTGCGAGGTGTAGAGCAATTTGCCA 485
OY 421 CTTCAATATGGAACCAAGTATTAAGAGTTTCCACATTTGGTTGGAATGATTAACA 480
Db 486 CTTCAATATGGAACCAAGTATTAAGAGTTTCCACATTTGGTTGGAATGATTAACA 545
OY 481 AGAAGCAAGTTGGGCTTCTAGTTTCTTTTGTCTGTACTGATGCAATTTATAGTCTG 540
Db 546 AGAAGCAAGTTGGGCTTCTAGTTTCTTTTGTCTGTACTGATGCAATTTATAGTCTG 605
OY 541 TCTTACCCCAATGAGCGATCTTACAGATTAACAAGTTGCTAACTGGGCATATCAACGTC 600
Db 606 TCTTACCCCAATGAGCGATCTTACAGATTAACAAGTTGCTAACTGGGCATATCAACGTC 665
OY 601 CAACAAATTAAGAAAGATGCTGAGTGAATGATGATTTGGAAGATGGAATTTATG 660
Db 666 CAACAAATTAAGAAAGATGCTGAGTGAATGATGATTTGGAAGATGGAATTTATG 725
OY 661 TCTCTGGGAATTTGGGATTTGGCAATATCTGGCTGTGTGCTGTGATCTATTCCATCT 720
Db 726 TCTCTGGGAATTTGGGATTTGGCAATATCTGGCTGTGTGCTGTGATCTATTCCATCT 785
OY 721 GTGAGTGACTCTTTGACATGAGAGAAATTCATATATTCAAGCAAGCTTAGAATGTT 780
Db 786 GTGAGTGACTCTTTGACATGAGAGAAATTCATATATTCAAGCAAGCTTAGAATGTT 845
OY 781 TCCCTTCTACTGGGCAATACACGATTTGTTTGGCTGGAATTAAGGATAGATATA 840
Db 846 TCCCTTCTACTGGGCAATACACGATTTGTTTGGCTGGAATTAAGGATAGATATA 905
OY 841 AAACAAATTTGATGATACCTCCAACTTTATGATAGCTGTTTCCCTCCAAATGTT 900
Db 906 AAACAAATTTGATGATACCTCCAACTTTATGATAGCTGTTTCCCTCCAAATGTT 965
OY 901 GTCTGATATTTAAAGCATATCTATTCCTGCAATGCTTGAAGAAATGTAAGATT 960
Db 966 GTCTGATATTTAAAGCATATCTATTCCTGCAATGCTTGAAGAAATGTAAGATT 1025
OY 961 AGACATGTTGGGAAGCGTCAACCAAAATTAACAAAATGAGATGTTCCAGTTG 1017
Db 1026 AGACATGTTGGGAAGCGTCAACCAAAATTAACAAAATGAGATGTTCCAGTTG 1082

RESULT 10
US-09-759-143-878
; Sequence 878, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Ronger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
```

```
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Patrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143-878

Query Match 100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 76-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGAAAGCAGAAAAGACATCAAAACCAAGAAGACTTTGAAAATGAGCCTAGAGA 60
Db 66 ATGGAAAGCAGAAAAGACATCAAAACCAAGAAGACTTTGAAAATGAGCCTAGAGA 125
OY 61 AATTTAAGAAAGAGATTAATTTGATTAAGACACGGAGAGACCGATCTAATAAGA 120
Db 126 AATTTAAGAAAGAGATTAATTTGATTAAGACACGGAGAGACCGATCTAATAAGA 185
OY 121 CCGTGTCTTTTGCATTTTGCACCAACACGCCATGTGATTAATTTGATGCGCCCTCAGAA 180
Db 186 CCGTGTCTTTTGCATTTTGCACCAACACGCCATGTGATTAATTTGATGCGCCCTCAGAA 245
OY 181 CTTGACGACACAGAACTCTTTCACAGTGGCACTTGCATTTAAATAGCTGCTATT 240
Db 246 CTTGACGACACAGAACTCTTTCACAGTGGCACTTGCATTTAAATAGCTGCTATT 305
OY 241 ATAGCATCTGACTTTTCTTTTACCTCTTCTGAGGGAAGTATTCACCTTTAGCACT 300
Db 306 ATAGCATCTGACTTTTCTTTTACCTCTTCTGAGGGAAGTATTCACCTTTAGCACT 365
OY 301 TCCCATCAACAATATTTTAAATTCGAATCTGTGCATCAACAAGTCTTGGCAATG 360
Db 366 TCCCATCAACAATATTTTAAATTCGAATCTGTGCATCAACAAGTCTTGGCAATG 425
OY 361 GTTTCATCACTCTCTGCAATTTGTTTAACTGCGAGGTGTAGAGCAATTTGCCA 420
Db 426 GTTTCATCACTCTCTGCAATTTGTTTAACTGCGAGGTGTAGAGCAATTTGCCA 485
OY 421 CTTCAATATGGAACCAAGTATTAAGAGTTTCCACATTTGGTTGGAATGATTAACA 480
Db 486 CTTCAATATGGAACCAAGTATTAAGAGTTTCCACATTTGGTTGGAATGATTAACA 545
OY 481 AGAAGCAAGTTGGGCTTCTAGTTTCTTTTGTCTGTACTGATGCAATTTATAGTCTG 540
Db 546 AGAAGCAAGTTGGGCTTCTAGTTTCTTTTGTCTGTACTGATGCAATTTATAGTCTG 605
OY 541 TCTTACCCCAATGAGCGATCTTACAGATTAACAAGTTGCTAACTGGGCATATCAACGTC 600
Db 606 TCTTACCCCAATGAGCGATCTTACAGATTAACAAGTTGCTAACTGGGCATATCAACGTC 665
OY 601 CAACAAATTAAGAAAGATGCTGAGTGAATGATGATTTGGAAGATGGAATTTATG 660
Db 666 CAACAAATTAAGAAAGATGCTGAGTGAATGATGATTTGGAAGATGGAATTTATG 725
OY 661 TCTCTGGGAATTTGGGATTTGGCAATATCTGGCTGTGTGCTGTGATCTATTCCATCT 720
Db 726 TCTCTGGGAATTTGGGATTTGGCAATATCTGGCTGTGTGCTGTGATCTATTCCATCT 785
OY 721 GTGAGTGACTCTTTCATGAGAGAAATTCATATATTCAAGCAAGCTTAGAATGTT 780
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Db 786 GTGAGTACTCTTTGACATGAGAGAAATTTCACTAATATTACAGCAAGCTAGAAATGTT 845
Qy 781 TCCCTTCTACTGGGACAAATACAGCAATTTGCTGGAATTAAGTATGATATA 840
Db 846 TCCCTTCTACTGGGACAAATACAGCAATTTGCTGGAATTAAGTATGATATA 905
Qy 841 AAACAATTTGATGATATACCTTCGAATTTATGATAGCTGTTTCTTCCAAATGTT 900
Db 906 AAACAATTTGATGATATACCTTCGAATTTATGATAGCTGTTTCTTCCAAATGTT 965
Qy 901 GTCTGATATTAAAGATATCTATCTGCGCATGCTTGAGAGAAAGATCTGAATTT 960
Db 966 GTCTGATATTAAAGATATCTATCTGCGCATGCTTGAGAGAAAGATCTGAATTT 1025
Qy 961 AGACATGTTGGAGAGAGCTGACCAAAATTAACAACTGATATGTTCCAGTTG 1017
Db 1026 AGACATGTTGGAGAGAGCTGACCAAAATTAACAACTGATATGTTCCAGTTG 1082

RESULT 11

US-09-780-669-878
Sequence 878, Application US/09780669
Patent No. US2002005197A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalo, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Veevick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FaSTSeq for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-780-669-878

Query Match 100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGAAGAGAGAAAGATCAAAACCAAGAAATTTGAAAATGAAGCTTAGAGAGA 60
Db 66 ATGGAAGAGAGAAAGATCAAAACCAAGAAATTTGAAAATGAAGCTTAGAGAGA 125
Qy 61 AATTGAGAGAGAGATTTATTTGCAATAGAGACCGGAGAGACCGAGATGCTTAAAGA 120
Db 126 AATTGAGAGAGAGATTTATTTGCAATAGAGACCGGAGAGACCGAGATGCTTAAAGA 185
Qy 121 CCGTGGCTTTGATTTGACCAAAAGAGCCGATGCTGATGAATTTGACGCTTCAAGA 180
Db 186 CCGTGGCTTTGATTTGACCAAAAGAGCCGATGCTGATGAATTTGACGCTTCAAGA 245

Qy 181 CTTAGACACACAGAGAACTCTTTCACAGTGGCACTTGGCAATTAATAAGTGTATT 240
Db 246 CTTAGACACACAGAGAACTCTTTCACAGTGGCACTTGGCAATTAATAAGTGTATT 305
Qy 241 ATAGCATCTGACTTTTCTTACCTCTTCAAGGAAATTAATCACTTTAGCACT 300
Db 306 ATAGCATCTGACTTTTCTTACCTCTTCAAGGAAATTAATCACTTTAGCACT 365
Qy 301 TCCATCAACAATTTTAAATTTCAATCTGATCAACAAAGCTTGGCAATG 360
Db 366 TCCATCAACAATTTTAAATTTCAATCTGATCAACAAAGCTTGGCAATG 425
Qy 361 GTTTCATCATCTCTTGGCATTTGTTACCTGCAAGGTGTATAGAGATTTGCCA 420
Db 426 GTTTCATCATCTCTTGGCATTTGTTACCTGCAAGGTGTATAGAGATTTGCCA 485
Qy 421 CTTCAATTAAGAGAACAGTTAAGAGATTTGCCAATTTGTTGATAGAGATTTA 480
Db 486 CTTCAATTAAGAGAACAGTTAAGAGATTTGCCAATTTGTTGATAGAGATTTA 545
Qy 481 AGAAGCAGTTGGGCTTCTCAGTTCTTTTGTCTGTACTGATGCAATTTTATGCTG 540
Db 546 AGAAGCAGTTGGGCTTCTCAGTTCTTTTGTCTGTACTGATGCAATTTTATGCTG 605
Qy 541 TCTTACCAGTGGGCTTCTCAGTTCTTTTGTCTGTACTGATGCAATTTTATGCTG 600
Db 606 TCTTACCAGTGGGCTTCTCAGTTCTTTTGTCTGTACTGATGCAATTTTATGCTG 665
Qy 601 CAACAAATTAAGAGAACAGTTAAGAGATTTGCCAATTTGTTGATAGAGATTTA 660
Db 666 CAACAAATTAAGAGAACAGTTAAGAGATTTGCCAATTTGTTGATAGAGATTTA 725
Qy 661 TCTGGAATTTGGGCTTCTCAGTTCTTTTGTCTGTACTGATGCAATTTTATGCTG 720
Db 726 TCTGGAATTTGGGCTTCTCAGTTCTTTTGTCTGTACTGATGCAATTTTATGCTG 785
Qy 721 GTGAGTACTCTTTGACATGAGAGAAATTTCACTAATATTACAGCAAGCTAGAAATGTT 780
Db 786 GTGAGTACTCTTTGACATGAGAGAAATTTCACTAATATTACAGCAAGCTAGAAATGTT 845
Qy 781 TCCCTTCTACTGGGACAAATACAGCAATTTGCTGGAATTAAGTATGATATA 840
Db 846 TCCCTTCTACTGGGACAAATACAGCAATTTGCTGGAATTAAGTATGATATA 905
Qy 841 AAACAATTTGATGATATACCTTCGAATTTATGATAGCTGTTTCTTCCAAATGTT 900
Db 906 AAACAATTTGATGATATACCTTCGAATTTATGATAGCTGTTTCTTCCAAATGTT 965
Qy 901 GTCTGATATTAAAGATATCTATCTGCGCATGCTTGAGAGAAAGATCTGAATTT 960
Db 966 GTCTGATATTAAAGATATCTATCTGCGCATGCTTGAGAGAAAGATCTGAATTT 1025
Qy 961 AGACATGTTGGAGAGAGCTGACCAAAATTAACAACTGATATGTTCCAGTTG 1017
Db 1026 AGACATGTTGGAGAGAGCTGACCAAAATTAACAACTGATATGTTCCAGTTG 1082

RESULT 12

US-09-822-827-878
Sequence 878, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalo, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Veevick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FaSTSeq for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA

ORGANISM: Homo sapiens
US-09-822-878

Query Match 100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1026 AGACATGTTGGGAAGCGTCACCAAAATTAACAACTGATATGTTCCAGTTG 1082

RESULT 13
US-09-895-793-878
; Sequence 878, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Ketter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 21021.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-878

Query Match 100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAAGCAGAAAAGACATCAACAAAGAACTTTGGAAAAATGAAGCTTAGAGA 60
DB 66 ATGGAAGCAGAAAAGACATCAACAAAGAACTTTGGAAAAATGAAGCTTAGAGA 125
QY 61 AATTAGAAGAGAGATATTTGCAATAAGAGACAGGGAGAGACCGATGCTAAAGAA 120
DB 126 AATTAGAAGAGAGATATTTGCAATAAGAGACAGGGAGAGACCGATGCTAAAGAA 185
QY 121 CCGTGCTTTTGCATTTGACCAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
DB 186 CCGTGCTTTTGCATTTGACCAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245
QY 181 CTTGACGACACACAGGAACCTCTTTCCACAGTGGCACTTCCCAATTAAATAGCTGTA 240
DB 246 CTTGACGACACACAGGAACCTCTTTCCACAGTGGCACTTCCCAATTAAATAGCTGTA 305
QY 241 ATAGATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGTAATTGACCCCTTAGCACT 300
DB 306 ATAGATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGTAATTGACCCCTTAGCACT 365
QY 301 TCCCATCAACAATATTTTATAAATTCATCTGTCATCAACAAGTCTTGGCCAA 360
DB 366 TCCCATCAACAATATTTTATAAATTCATCTGTCATCAACAAGTCTTGGCCAA 425
QY 361 GTTTCATGACTCTCTTGGCATTTGTTACCTGCCAGGTGTATGACACCAATTGCCAA 420
DB 426 GTTTCATGACTCTCTTGGCATTTGTTACCTGCCAGGTGTATGACACCAATTGCCAA 485
QY 421 CTTCAATATGAGAACCAAGTATAGAGAGTTTCCACATTTGGTGAATAGATGTTAACA 480
DB 486 CTTCAATATGAGAACCAAGTATAGAGAGTTTCCACATTTGGTGAATAGATGTTAACA 545
QY 481 AGAAGCAGTTTGGGCTCTCACTTTCTTTTGTCTGTACTGATGCAATTTATAGCTG 540
DB 546 AGAAGCAGTTTGGGCTCTCACTTTCTTTTGTCTGTACTGATGCAATTTATAGCTG 605
QY 541 TCTTACCCATGAGCGGATCTTACAGATACAAAGTCTTAACTGGGCAATCAACAGGTC 600
DB 606 TCTTACCCATGAGCGGATCTTACAGATACAAAGTCTTAACTGGGCAATCAACAGGTC 665
QY 601 CAACAAAATAAGAGAGATGCTGGATTTGAGCATGATTTGGAGATGAGATTTATG 660
DB 666 CAACAAAATAAGAGAGATGCTGGATTTGAGCATGATTTGGAGATGAGATTTATG 725
QY 661 TCTCTGGAATTTGGGATTTGGCAATCTGCTTGGCTGTAATCTATTCATCT 720
DB 726 TCTCTGGAATTTGGGATTTGGCAATCTGCTTGGCTGTAATCTATTCATCT 785
QY 721 GTGAGTGAATCTTTGACATGAGAGAAATTTCACTATTTCAAGCAAGCTAGGAATTT 780
DB 786 GTGAGTGAATCTTTGACATGAGAGAAATTTCACTATTTCAAGCAAGCTAGGAATTT 845
QY 781 TCCCTCTCTGCGGCAATPACGAGATTTTGGCTGGAGTAAGTATGATATTA 840
DB 846 TCCCTCTCTGCGGCAATPACGAGATTTTGGCTGGAGTAAGTATGATATTA 905
QY 841 AAACAATTTGTATGATACCTCCAACTTTTATGATAGCTGTTTCTTCCAAATGTT 900
DB 906 AAACAATTTGTATGATACCTCCAACTTTTATGATAGCTGTTTCTTCCAAATGTT 965
QY 901 GTTCGTATTTTAAAGCATATTTCTGCGCATGCTTGAAGAGAAAGATCTGAAGATT 960
DB 966 GTTCGTATTTTAAAGCATATTTCTGCGCATGCTTGAAGAGAAAGATCTGAAGATT 1025
QY 961 AGACATGTTGGGAAGCGTCACCAAAATTAACAACTGATATGTTCCAGTTG 1017

QY 1 ATGGAAGCAGAAAAGACATCAACAAAGAACTTTGGAAAAATGAAGCTTAGAGA 60
DB 66 ATGGAAGCAGAAAAGACATCAACAAAGAACTTTGGAAAAATGAAGCTTAGAGA 125
QY 61 AATTAGAAGAGAGATATTTGCAATAAGAGACAGGGAGAGACCGATGCTAAAGAA 120
DB 126 AATTAGAAGAGAGATATTTGCAATAAGAGACAGGGAGAGACCGATGCTAAAGAA 185
QY 121 CCGTGCTTTTGCATTTGACCAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
DB 186 CCGTGCTTTTGCATTTGACCAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245
QY 181 CTTGACGACACACAGGAACCTCTTTCCACAGTGGCACTTCCCAATTAAATAGCTGTA 240
DB 246 CTTGACGACACACAGGAACCTCTTTCCACAGTGGCACTTCCCAATTAAATAGCTGTA 305
QY 241 ATAGATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGTAATTGACCCCTTAGCACT 300
DB 306 ATAGATCTCTGACTTTTCTTTACACTCTTCTGAGGGAGTAATTGACCCCTTAGCACT 365
QY 301 TCCCATCAACAATATTTTATAAATTCATCTGTCATCAACAAGTCTTGGCCAA 360
DB 366 TCCCATCAACAATATTTTATAAATTCATCTGTCATCAACAAGTCTTGGCCAA 425
QY 361 GTTTCATGACTCTCTTGGCATTTGTTACCTGCCAGGTGTATGACACCAATTGCCAA 420

Db 426 GTTTCATCACTCTCTTGCGATTGGTTTACCTGCGAGGTGTATAGACGAATTGTCCAA 485
Qy 421 CTTCAATATGGAACCAAGTATTAAGAGTTTCCACATTTGGTATGATGATGATTAACA 480
Db 486 CTTCAATATGGAACCAAGTATTAAGAGTTTCCACATTTGGTATGATGATGATTAACA 545
Qy 481 AGAAGACGTTGGGCTTCTCAAGTTCTTTTGTCTGTACTGCATGCAATTTATAGTCTG 540
Db 546 AGAAGACGTTGGGCTTCTCAAGTTCTTTTGTCTGTACTGCATGCAATTTATAGTCTG 605
Qy 541 TCTTACCCATGAGGCGATCTCAGATACAGATGTTGTAACCTGGGATATCAACAGTCT 600
Db 606 TCTTACCCATGAGGCGATCTCAGATACAGATGTTGTAACCTGGGATATCAACAGTCT 665
Qy 601 CAACAAATTAAGAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db 666 CAACAAATTAAGAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 725
Qy 661 TCTCTGGGAATTTGGGATTTGGCAATACCTGCTGTGGCTGTGACATCTATTCCACT 720
Db 726 TCTCTGGGAATTTGGGATTTGGCAATACCTGCTGTGGCTGTGACATCTATTCCACT 785
Qy 721 GTGAGTGAATCTTTGACATGAGAGAAATTTCACTATTTTCAAGCAAGCTAGAGATTTGT 780
Db 786 GTGAGTGAATCTTTGACATGAGAGAAATTTCACTATTTTCAAGCAAGCTAGAGATTTGT 845
Qy 781 TCCCTTCTACTGGGCAATACAGCATGATTTTGGCTGGAATTAAGTATGATGATGATG 840
Db 846 TCCCTTCTACTGGGCAATACAGCATGATTTTGGCTGGAATTAAGTATGATGATGATG 905
Qy 841 AAACAATTTGTATGATATACACTCCCACTTTTATGATGATGATGATGATGATGATG 900
Db 906 AAACAATTTGTATGATATACACTCCCACTTTTATGATGATGATGATGATGATGATG 965
Qy 901 GTCCGATATTTTAAAGCATATCTTCTGCGCATGCTTGGAGAGAAAGATCTGAAGATT 960
Db 966 GTCCGATATTTTAAAGCATATCTTCTGCGCATGCTTGGAGAGAAAGATCTGAAGATT 1025
Qy 961 AGACATGTTGGGAGACGTCACCAAAATTAACAAAAGTATGATGATGATGATGATG 1017
Db 1026 AGACATGTTGGGAGACGTCACCAAAATTAACAAAAGTATGATGATGATGATGATG 1082

RESULT 14
US-09-895-814-878
; Sequence 878, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yaeli A.W.
; APPLICANT: Hepley, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26

; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-878

Query Match 100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAAGACAGAAACATCAACCAAGAACTTTGGAATTAAGAGCTTAGAGAG 60
Db 66 ATGGAAGACAGAAACATCAACCAAGAACTTTGGAATTAAGAGCTTAGAGAG 125
Qy 61 AATTGAGAGAGACGATTTTGTATAGAGACCGGAGAGACGACATGCTAAAAAGA 120
Db 126 AATTGAGAGAGAGATTTTGTATAGAGACCGGAGAGACGACATGCTAAAAAGA 185
Qy 121 CCGTGTCTTTTGCATTTGACACCAACAGCCCATGCTGATGAATTTGACTGCCCTCAGAA 180
Db 186 CCGTGTCTTTTGCATTTGACACCAACAGCCCATGCTGATGAATTTGACTGCCCTCAGAA 245
Qy 181 CTTGACACACAGGAACTTTTCCAGAGTGGCACTTGGCAATTTAAATAGCTGATTT 240
Db 246 CTTGACACACAGGAACTTTTCCAGAGTGGCACTTGGCAATTTAAATAGCTGATTT 305
Qy 241 ATAGCATCTGACTTTTCTTATACACTCTTCTGAGGAGAAATTAATCACTTTAGCACT 300
Db 306 ATAGCATCTGACTTTTCTTATACACTCTTCTGAGGAGAAATTAATCACTTTAGCACT 365
Qy 301 TCCCATCAACAAATTTTATTAATTTCCAACTCTGCTGATCATCAACAACTTTGCCAATG 360
Db 366 TCCCATCAACAAATTTTATTAATTTCCAACTCTGCTGATCATCAACAACTTTGCCAATG 425
Qy 361 GTTTCATGACTCTGTGGCATTTGTTTACCTGCGCAGAGTGTATGCGCAATTTGCCAA 420
Db 426 GTTTCATGACTCTGTGGCATTTGTTTACCTGCGCAGAGTGTATGCGCAATTTGCCAA 485
Qy 421 CTTCAATATGGAACCAAGTATTAAGAGTTTCCACATTTGGTATGATGATGATTAACA 480
Db 486 CTTCAATATGGAACCAAGTATTAAGAGTTTCCACATTTGGTATGATGATGATTAACA 545
Qy 481 AGAAGACGTTGGGCTTCTCAAGTTCTTTTGTCTGTACTGCATGCAATTTATAGTCTG 540
Db 546 AGAAGACGTTGGGCTTCTCAAGTTCTTTTGTCTGTACTGCATGCAATTTATAGTCTG 605
Qy 541 TCTTACCCATGAGGCGATCTCAGATACAGATGTTGTAACCTGGGATATCAACAGTCT 600
Db 606 TCTTACCCATGAGGCGATCTCAGATACAGATGTTGTAACCTGGGATATCAACAGTCT 665
Qy 601 CAACAAATTAAGAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db 666 CAACAAATTAAGAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 725
Qy 661 TCTCTGGGAATTTGGGATTTGGCAATACCTGCTGTGGCTGTGACATCTATTCCACT 720
Db 726 TCTCTGGGAATTTGGGATTTGGCAATACCTGCTGTGGCTGTGACATCTATTCCACT 785
Qy 721 GTGAGTGAATCTTTGACATGAGAGAAATTTCACTATTTTCAAGCAAGCTAGAGATTTGT 780
Db 786 GTGAGTGAATCTTTGACATGAGAGAAATTTCACTATTTTCAAGCAAGCTAGAGATTTGT 845
Qy 781 TCCCTTCTACTGGGCAATACAGCATGATTTTGGCTGGAATTAAGTATGATGATTA 840
Db 846 TCCCTTCTACTGGGCAATACAGCATGATTTTGGCTGGAATTAAGTATGATGATTA 905
Qy 841 AAACAATTTGTATGATATACACTCCCACTTTTATGATGATGATGATGATGATGATG 900
Db 906 AAACAATTTGTATGATATACACTCCCACTTTTATGATGATGATGATGATGATGATG 965

OY	901	ATCCGTAATATTAAAGATCTACTTCTCGCATCTTGAGGAAGAATACTGAAGTT	960
Db	966	GTCCTGATTTTAAAGACATCACTATTCCTGCCATCTTGAGGAAGAATACTGAAGTT	1025
OY	961	AGACATGTTGGGAAGACGTCAACCMAATTAAACAACACTGAGATATGTTCCCACTTG	1017
db	1026	AGACATGTTGGGAAGACGTCAACCMAATTAAACAACACTGAGATATGTTCCCACTTG	1082

RESULT 15
US-10-012-896-878
; Sequence 878, Application US/10012896
; Publication No. US20020183251A1

GENERAL INFORMATION:

```

/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, David C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yugu
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedrick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel X.
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yaeli A.W.
/ APPLICANT: Hepfer, William T.
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Hurai, John
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: Vinals de Bassols, Carlota
/ APPLICANT: Foy, Teresa
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Wantanabe, Yoshinori
/ APPLICANT: Meagher, Madeleine Joy
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C27
/ CURRENT APPLICATION NUMBER: US/10/012,896
/ CURRENT FILING DATE: 2001-12-10
/ NUMBER OF SEQ ID NOS: 1011
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 878
/ LENGTH: 1195
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-012-896-878

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Query Match	Score	DB	Length
100.0%	1017	5	1195

Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY	1	ATGGAAGAGCAAAAACAATCAACAAACCAAGAACTTTGGAAATGAAAGCCTACGAGA	60
Db	66	ATGGAAGAGCAAAAACAATCAACAAACCAAGAACTTTGGAAATGAAAGCCTACGAGA	125
QY	61	AATTTGAGAAGACGATTATTTGGCATTAAGSACACGGAGAGACGACATGCTAAAGA	120
Db	126	AATTTGAGAAGACGATTATTTGGCATTAAGSACACGGAGAGACGACATGCTAAAGA	185
QY	121	CCTGTCCTTTGGCATTTGCACAAACAGCCCATGCTGATGAATTTGACATGCCCTTCAGAA	180
Db	186	CCTGTCCTTTGGCATTTGCACAAACAGCCCATGCTGATGAATTTGACATGCCCTTCAGAA	245
QY	181	CTTCACACACACAGGAACCTTTCCACAGTGCACCTTGGCAATTAATAATAGCTGTATT	240
Db	246	CTTCACACACACAGGAACCTTTCCACAGTGCACCTTGGCAATTAATAATAGCTGTATT	305
QY	241	ATAGCATCTCGACTTTTCTTAACTCTTTGAGGAGATTAATCAACCTTTAGCACT	300

Db	306	ATAGCATCTCGACTTTTCTTTTACACTCTTGTGGSAAAGTAATTCACCCCTTAGCAACT	365
QY	301	TCCGATCAACAATTTTATTAATAATCCAAATCCTGTCTATCAACAAGTCTTGCCAAATG	360
Db	366	TCCCATCAACAATTTTATTAATAATCCAAATCCTGTCTATCAACAAGTCTTGCCAAATG	425
QY	361	GTTCGCATCTCTCTTGGCATTGGTTTACCTGCGAGGTGTGATGACGAATGTGCCAA	420
Db	426	GTTCGCATCTCTCTTGGCATTGGTTTACCTGCGAGGTGTGATGACGAATGTGCCAA	485
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Db	546	AGAAAGCAGTTGGGCTCTCAGTTTCTTTTTCCTGTACTGCATGCATGCAATTTATAGTCG	605
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QY	601	CAACAAATTAAGAAGATGCTGTGATTTGAGCATGATGTTTGAGATATGAGATTTATGTG	660
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QY	661	TCTCTGGGAATTTGGGAAATTTGGCAATCTGTGCTCTGTTGGCTGTGACATCTATTCACACT	720
Db	726	TCTCTGGGAATTTGGGAAATTTGGCAATCTGTGCTCTGTTGGCTGTGACATCTATTCACACT	785
QY	721	GTGAGTGCCTCTTTGACATGAGAGGAATTCACATATTCAGAGCAAGCTAGGAATTTGT	780
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QY	781	TCCCTTCTACTGGGACACAATACAGCAATGATTTTTTGTGCTGGAATTAAGTGATATGATTA	840
Db	846	TCCCTTCTACTGGGACACAATACAGCAATGATTTTTTGTGCTGGAATTAAGTGATATGATTA	905
QY	841	AAACAAATTTGATGATATACACTTCCAACTTTTATGATAGCTGTTTCTCTTCCAAATTTGT	900
Db	906	AAACAAATTTGATGATATACACTTCCAACTTTTATGATAGCTGTTTCTCTTCCAAATTTGT	965
QY	901	GTCTCGATATTTAAAGCATACTATTTCTGCGCATGCTTTGAGAGGAAGAAATCTGAAAGTT	960
Db	966	GTCTCGATATTTAAAGCATACTATTTCTGCGCATGCTTTGAGAGGAAGAAATCTGAAAGTT	1025
QY	961	AGACAATGTTGGGAAGAGCTCACCAAAATTTAACAAACCTGAGATATGTTTCCCAAGTTG	1017
Db	1026	AGACAATGTTGGGAAGAGCTCACCAAAATTTAACAAACCTGAGATATGTTTCCCAAGTTG	1082

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Job time : 952.415 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2005, 20:43:36 ; Search time 202.756 Seconds
(without alignments)
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Title: US-10-750-262-1_COPY_66_1082

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Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1017	100.0	1193	US-09-455-486-1	Sequence 1, Appli
2	1017	100.0	1195	US-09-323-873A-1	Sequence 1, Appli
3	1017	100.0	1195	US-09-685-166A-878	Sequence 878, App
4	1017	100.0	1195	US-09-679-426-878	Sequence 878, App
5	1017	100.0	1195	US-09-759-143-878	Sequence 878, App
6	1017	100.0	1195	US-10-010-667A-1	Sequence 1, Appli
7	1017	100.0	1195	US-10-012-896-878	Sequence 878, App
8	1015.4	99.8	1147	US-09-949-016-2686	Sequence 2686, Ap
9	760.6	74.8	3627	US-09-323-873A-6	Sequence 6, Appli
10	760.6	74.8	3627	US-09-455-486-4	Sequence 4, Appli
11	760.6	74.8	3627	US-10-010-667A-6	Sequence 6, Appli
12	516	50.7	592	US-09-439-313-342	Sequence 342, App
13	516	50.7	592	US-09-352-616A-342	Sequence 342, App
14	516	50.7	592	US-09-636-215-342	Sequence 342, App
15	516	50.7	592	US-09-685-166A-342	Sequence 342, App
16	516	50.7	592	US-09-679-426-342	Sequence 342, App
17	516	50.7	592	US-09-759-143-342	Sequence 342, App
18	516	50.7	592	US-09-651-236-342	Sequence 342, App
19	516	50.7	592	US-09-657-279-342	Sequence 342, App
20	516	50.7	592	US-10-012-896-342	Sequence 342, App
21	515.6	50.7	9073	US-09-949-016-14428	Sequence 14428, A
22	266.6	26.2	2453	US-09-455-486-5	Sequence 5, Appli
23	266.6	26.2	2469	US-10-104-047-1185	Sequence 1185, App
24	265	26.1	1403	US-10-012-896-995	Sequence 995, App

25	256.8	25.3	455	3	US-09-621-976-9264	Sequence 9264, Ap
26	229.6	22.6	848	3	US-10-012-896-993	Sequence 993, App
27	221.4	21.8	519	3	US-10-010-667A-7	Sequence 7, Appli
28	221.4	21.8	521	3	US-09-323-873A-7	Sequence 7, Appli
29	212.8	20.9	2714	3	US-09-562-930-5	Sequence 5, Appli
30	212.8	20.9	3884	3	US-09-562-930-10	Sequence 10, Appli
31	187.4	18.4	4429	3	US-09-455-486-7	Sequence 7, Appli
32	184.8	18.2	1213	3	US-09-083-521-3	Sequence 3, Appli
33	171	16.8	1886	3	US-09-562-930-1	Sequence 1, Appli
34	166.6	16.4	1203	3	US-09-544-618-6	Sequence 6, Appli
35	162.4	16.0	366	3	US-09-030-607-215	Sequence 215, App
36	162.4	16.0	366	3	US-09-439-313-215	Sequence 215, App
37	162.4	16.0	366	3	US-09-352-616A-215	Sequence 215, App
38	162.4	16.0	366	3	US-09-232-149A-215	Sequence 215, App
39	162.4	16.0	366	3	US-09-159-812-215	Sequence 215, App
40	162.4	16.0	366	3	US-09-636-215-215	Sequence 215, App
41	162.4	16.0	366	3	US-09-685-166A-215	Sequence 215, App
42	162.4	16.0	366	3	US-09-115-453-215	Sequence 215, App
43	162.4	16.0	366	3	US-09-688-489-215	Sequence 215, App
44	162.4	16.0	366	3	US-09-679-426-215	Sequence 215, App
45	162.4	16.0	366	3	US-09-759-143-215	Sequence 215, App

ALIGNMENTS

RESULT 1
US-09-455-486-1
Sequence 1, Application US/09455486
Patent No. 6833438
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Seifman
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
FILE REFERENCE: 129.17-US-11
CURRENT APPLICATION NUMBER: US/09/455,486
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1193
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (64)...(1083)
US-09-455-486-1
Query Match 100.0%; Score 1017; DB 3; Length 1193;
Best Local Similarity 100.0%; Pred. No. 2.5e-304;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db QY 1 ATGGAAGCGAAGACATCAACCAAGAAAGACTTTGGAAAAATGAAGCCTTAGAGA 60
64 ATGGAAGCGAAGAAAGCATCAACCAAGAAAGACTTTGGAAAAATGAAGCCTTAGAGA 123
QY 61 AATTAGAGAGAGCATTTATTTGCTATAGAGACAGGAGAGACACAGATGCTTAAAGA 120
124 AATTAGAGAGAGCATTTATTTGCTATAGAGACAGGAGAGACACAGATGCTTAAAGA 183
QY 121 CTTGTGCTTTGCAATTTGCAACCAAGCCATGCTGATGAATTTGACTGCTTCAAGAA 180
184 CTTGTGCTTTGCAATTTGCAACCAAGCCATGCTGATGAATTTGACTGCTTCAAGAA 243
QY 181 CTTGAGACACACAGAACTCTTTCCACATGTCGACTTGGCAATTAATAGCGCATTT 240
244 CTTGAGACACACAGAACTCTTTCCACATGTCGACTTGGCAATTAATAGCGCATTT 303

QY 241 ATAGCATCTGCACTTTCTTTACACTCTCTGAGGAGAAATTCACCCCTTAGCAACT 300
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Db 304 ATAGCATCTGCACTTTCTTTACACTCTCTGAGGAGAAATTCACCCCTTAGCAACT 363
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QY 301 TCCCATCAACAATTTTATTAATAATTCGAATCTGCTCATCAACAAAGCTTGGCCATG 360
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Db 364 TCCCATCAACAATTTTATTAATAATTCGAATCTGCTCATCAACAAAGCTTGGCCATG 423
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QY 361 GTTTCATCACTCTCTTGGAGATTGGTTTACCTGACAGTGTGATAGAGAAATTTGCCAA 420
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Db 424 GTTTCATCACTCTCTTGGAGATTGGTTTACCTGACAGTGTGATAGAGAAATTTGCCAA 483
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QY 421 CTTCATATATGAACCAAGTATTAAGAAGTTTCCATTTGGTGTGATTAAGATTTTAAACA 480
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Db 484 CTTCATATATGAACCAAGTATTAAGAAGTTTCCATTTGGTGTGATTAAGATTTTAAACA 543
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QY 481 AGAAGACAGTTTGGGCTTCTCAAGTTCTTTTGTCTGTACTGCATGCAATTTATAGCTG 540
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Db 544 AGAAGACAGTTTGGGCTTCTCAAGTTCTTTTGTCTGTACTGCATGCAATTTATAGCTG 603
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QY 541 TCTTACCCATATGAGGAGATCTCTACAGTATACAGTTGCTAACTGGGAGATTCACAGGCTC 600
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Db 604 TCTTACCCATATGAGGAGATCTCTACAGTATACAGTTGCTAACTGGGAGATTCACAGGCTC 663
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QY 601 CAACAAATTAAGAAGATGCTGGAATTCAGATGATTTTGGAGAAATGAGATTTATGTG 660
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RESULT 2
US-09-323-873A-1
; Sequence 1, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; FILE REFERENCE: 129.16USU2
; CURRENT APPLICATION NUMBER: US/09/323,873A
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183

; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-323-873A-1
Query Match 100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred No.2.5e-304;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 66 ATGGAAGAGAAAGACATCAACAACCAAGAAATTTGGAAATGAAGCTTAGAGAG 125
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 Db 966 GTCCGATATTTAAAGACATCTATTCTGCGATGCTTGAGAGAAATATCTGAAGTT 1025
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 QY 961 AGACATGTTGGGAAGACGTACCAAAATTAACAAATGTGATATGTTTCCCAAGTG 1017
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 Db 1026 AGACATGTTGGGAAGACGTACCAAAATTAACAAATGTGATATGTTTCCCAAGTG 1082
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RESULT 3

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Sequence 678. Application US/09685166A
Parent No. 6630305

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocke, Susan L.
APPLICANT: Jiang, Yuguai
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skolky, Yaeli A.W.
APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-685-166A-878

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Query Match	100.0%;	Score 1017;	DB 3;	Length 1195;
Best Local Similarity	100.0%;	Pred. No. 2,56-304;		
Matches 1017;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	66	ATGMAAGACGAAAAAGACATCA	CAAAACCAAGAAACTTTGGAAATGAAGCTTGAGAGA	125
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Db	126	AATTTAGAAAGAGCATTTATTTGGATA	GAACAAGAGAGACAGAGATGCTTAAAGA	185
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Db	186	CCTGGCTTTTGGACATTTTGACCA	CAACCCATGCTGATGAATTTGA	CTGCCCTTCAGAA 245
QY	181	CTTGACACACACAGAACTCTTTC	CACAGTGGCACTTGCCAATTTAAATATGACTGATTT 240	
Db	246	CTTGACACACACAGAACTCTTTC	CACAGTGGCACTTGCCAATTTAAATATGACTGATTT 305	
QY	241	ATAGATCTTGACCTTTCTTTTAC	CTCTTCTGAGGAAAGTAACTACCCCTTTAGCACT 300	
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Db	366	TCCCATCAACAATATTTTAAAT	TTAAATTCCAATCTGGTCATCAACAAGCTTTGCAATG 425	
QY	361	GTTCCTCATCACTCTCTTGACAT	TGGTTTAACTGACAGGTGATGACAGCAATGTCCAA 420	

Db	426	GTTCATCACTCTCTTGGAATGGTTTACCTGGCAGGTGATAGCAGCAATTGTCCAA	485
OY	421	CTTCATTAATGGAACCAAGTATTAAGAATTTCCAAATTTGGTGGATTAAGTGAATGTAA	480
Db	486	CTTATATATGGAACCAAGTATTAAGAATTTCCAAATTTGGTGGATTAAGTGAATGTAA	545
OY	481	AGAAAGCAGTTGGGCTTCTCAGTTCTGTTTTCCTTACTGATGCATGCATTTATAGTCG	540
Db	546	AGAAAGCAGTTGGGCTTCTCAGTTCTGTTTTCCTTACTGATGCATGCATTTATAGTCG	605
OY	541	TCTTAACCAATGAGCCGATCTTACAGATCAAGTTGCTTAAATGGGCATATCAACAGTC	600
Db	606	TCTTAACCAATGAGCCGATCTTACAGATCAAGTTGCTTAAATGGGCATATCAACAGTC	665
OY	601	CAACAAATAAAGAAGATGCTGATTTGAGCATGATTTGGAGATGAGATTTATGTG	660
Db	666	CAACAAATAAAGAAGATGCTGATTTGAGCATGATTTGGAGATGAGATTTATGTG	725
OY	661	TCTCTGGGAATTTGGGAATTTGGCAATACGTGCTCTGTTGGCTGTGACATCTAATTCACCT	720
Db	726	TCTCTGGGAATTTGGGAATTTGGCAATACGTGCTCTGTTGGCTGTGACATCTAATTCACCT	785
OY	721	GTGAGTGACTTTTGACATGGAGGAATTTACTATATTAGAGCAAGCTAGCAATGTT	780
Db	786	GTGAGTGACTTTTGACATGGAGGAATTTACTATATTAGAGCAAGCTAGCAATGTT	845
OY	781	TCCCTTCTACTGGGACAAATACAGCAATGATTTTTGCTGGAAATTAAGTGAATGATATA	840
Db	846	TCCCTTCTACTGGGACAAATACAGCAATGATTTTTGCTGGAAATTAAGTGAATGATATA	905
OY	841	AAACAATTTGATGATGTATACACCTCCAACTTTATGATAGCTGTTTCTTCCCAATGTT	900
Db	906	AAACAATTTGATGATGTATACACCTCCAACTTTATGATAGCTGTTTCTTCCCAATGTT	965
OY	901	GTCTGTATTTAAAGCATATCTATTCTCGCATGCTTGAGAGAAAGATATCTAAGATT	960
Db	966	GTCTGTATTTAAAGCATATCTATTCTCGCATGCTTGAGAGAAAGATATCTAAGATT	1025
OY	961	AGACATGTTGGGAAGACGTACCAAAATTTAACAAATCTGATATATGTTCCCAAGTTG	1017
Db	1026	AGACATGTTGGGAAGACGTACCAAAATTTAACAAATCTGATATATGTTCCCAAGTTG	1082

RESULT 4

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US-09-679-426-878
Sequence 878, Application US/09679426
Patent No. 6759515
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: POSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER.
FILE REFERENCE: 210121.427020
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: PaSeq for Windows Version 3.0

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; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-679-426-878

Query Match      100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.5e-304;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGGAAGCAGAAAGACATCACAAACCAAGAACTTTGGAAAATGAAGCTTAGAGA 60
      66 ATGGAAGCAGAAAGACATCACAAACCAAGAACTTTGGAAAATGAAGCTTAGAGA 125
QY      61 AATTGAAGAAAGACGATTAATTGCAATAGAGACAGGAGAGACAGCATGCTAAAAAGA 120
      126 AATTGAAGAAAGACGATTAATTGCAATAGAGACAGGAGAGACAGCATGCTAAAAAGA 185
QY      121 CCTGTGCTTTTGCAATTTTGACCAAAAGCCCATGCTGATGAATTTGACTGCCCTTGAAA 180
      186 CCTGTGCTTTTGCAATTTTGACCAAAAGCCCATGCTGATGAATTTGACTGCCCTTGAAA 245
QY      181 CTTCAGACACACAGGAACTCTTCCACAGTGGCACTTGGCAATTAATAATAGCTGAT 240
      246 CTTCAGACACACAGGAACTCTTCCACAGTGGCACTTGGCAATTAATAATAGCTGAT 305
QY      241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAATTAATCAACCTTTAGCACT 300
      306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAATTAATCAACCTTTAGCACT 365
QY      301 TCCCATCAACAATTTTATTAATAATTCGAATCTGTGATCAACAAGCTTTGCCAATG 360
      366 TCCCATCAACAATTTTATTAATAATTCGAATCTGTGATCAACAAGCTTTGCCAATG 425
QY      361 GTTTCATCACTCTCTGGCATTTGTTTACCTGCCAGTGTGATAGAGCAATTTGCCAA 420
      426 GTTTCATCACTCTCTGGCATTTGTTTACCTGCCAGTGTGATAGAGCAATTTGCCAA 485
QY      421 CTTCATATGGAACCAAGTATGAAGATTTCACATTTGTTGATTAAGTATTAACA 480
      486 CTTCATATGGAACCAAGTATGAAGATTTCACATTTGTTGATTAAGTATTAACA 545
QY      481 AGAAGACAGTTGGGCTTCTCAATTTCTTTTGGCTGATGATGCAATTTATGCTG 540
      546 AGAAGACAGTTGGGCTTCTCAATTTCTTTTGGCTGATGATGCAATTTATGCTG 605
QY      541 TCTTACCACATGAGGAGATCTTACAGATTCAGATTGCTAACTGGGCATATCAACAGGTC 600
      606 TCTTACCACATGAGGAGATCTTACAGATTCAGATTGCTAACTGGGCATATCAACAGGTC 665
QY      601 CAACAAATTAAGAAAGATGCTGATGATGATGATGATGATGATGATGATGATG 660
      666 CAACAAATTAAGAAAGATGCTGATGATGATGATGATGATGATGATGATGATG 725
QY      661 TCTCTGGGAATTTGGGATTTGGCAATAGCTGCTGTTGGCTGATGATGATGATGAT 720
      726 TCTCTGGGAATTTGGGATTTGGCAATAGCTGCTGTTGGCTGATGATGATGATGAT 785
QY      721 GTGAGTGAATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
      786 GTGAGTGAATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 845
QY      781 TCCCTTTCTAAGGAGCAATATACAGCATGATTTTGGCTGATTAAGTATGATGAT 840
      846 TCCCTTTCTAAGGAGCAATATACAGCATGATTTTGGCTGATTAAGTATGATGAT 905
QY      841 AAAACAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
      906 AAAACAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 965
QY      901 GTTCGATATTTAAAGCATATATCTGCGCATGCTTGAAGAAAGATATGCAAGAT 960
      966 GTTCGATATTTAAAGCATATATCTGCGCATGCTTGAAGAAAGATATGCAAGAT 1025
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QY      961 AGACATGTTGGAGAGACGTCACCAAAATTAACAAAATGAGATATGTTCCAGTTG 1017
      1026 AGACATGTTGGAGAGACGTCACCAAAATTAACAAAATGAGATATGTTCCAGTTG 1082

RESULT 5
US-09-759-143-878
Sequence 878, Application US/09759143
Patent No. 6800746
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuxi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick L.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143-878

Query Match      100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.5e-304;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGGAAGCAGAAAGACATCACAAACCAAGAACTTTGGAAAATGAAGCTTAGAGA 60
      66 ATGGAAGCAGAAAGACATCACAAACCAAGAACTTTGGAAAATGAAGCTTAGAGA 125
QY      61 AATTGAAGAAAGACGATTAATTGCAATAGAGACAGGAGAGACAGCATGCTAAAAAGA 120
      126 AATTGAAGAAAGACGATTAATTGCAATAGAGACAGGAGAGACAGCATGCTAAAAAGA 185
QY      121 CCTGTGCTTTTGCAATTTTGACCAAAAGCCCATGCTGATGAATTTGACTGCCCTTGAAA 180
      186 CCTGTGCTTTTGCAATTTTGACCAAAAGCCCATGCTGATGAATTTGACTGCCCTTGAAA 245
QY      181 CTTCAGACACACAGGAACTCTTCCACAGTGGCACTTGGCAATTAATAATAGCTGAT 240
      246 CTTCAGACACACAGGAACTCTTCCACAGTGGCACTTGGCAATTAATAATAGCTGAT 305
QY      241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAATTAATCAACCTTTAGCACT 300
      306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAATTAATCAACCTTTAGCACT 365
QY      301 TCCCATCAACAATTTTATTAATAATTCGAATCTGTGATCAACAAGCTTTGCCAATG 360
      366 TCCCATCAACAATTTTATTAATAATTCGAATCTGTGATCAACAAGCTTTGCCAATG 425
QY      361 GTTTCATCACTCTCTGGCATTTGTTTACCTGCCAGTGTGATAGAGCAATTTGCCAA 420
      426 GTTTCATCACTCTCTGGCATTTGTTTACCTGCCAGTGTGATAGAGCAATTTGCCAA 485
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QY 421 CTTCAATATGGAACCAAGTATGAAGATTCCACATTGGTTGATTAAGATGTTAACA 480
| | | | |
Db 486 CTTCAATATGGAACCAAGTATGAAGATTCCACATTGGTTGATTAAGATGTTAACA 545
| | | | |
QY 481 AGAAGACATTTGGGCTTCTCAAGTTCTTTTGGCTGATCTGATGCAATTTATAGTCTG 540
| | | | |
Db 546 AGAAGACATTTGGGCTTCTCAAGTTCTTTTGGCTGATCTGATGCAATTTATAGTCTG 605
| | | | |
QY 541 TCTTACCCATGAGGCGATCTCAGATACAGTTGCTAACTGGGCAATCAACAGTCT 600
| | | | |
Db 606 TCTTACCCATGAGGCGATCTCAGATACAGTTGCTAACTGGGCAATCAACAGTCT 665
| | | | |
QY 601 CAACAAATTAAGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 660
| | | | |
Db 666 CAACAAATTAAGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 725
| | | | |
QY 661 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGTGATCTTATCCATCT 720
| | | | |
Db 726 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGTGATCTTATCCATCT 785
| | | | |
QY 721 GTGAGTGAATCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATGTT 780
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Db 786 GTGAGTGAATCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATGTT 845
| | | | |
QY 781 TCCCTTCTACTGGGCAATATACAGCAATGATTTTGGCTGAAATAGTGAATGATATAT 840
| | | | |
Db 846 TCCCTTCTACTGGGCAATATACAGCAATGATTTTGGCTGAAATAGTGAATGATATAT 905
| | | | |
QY 841 AAACAAATTTGATGATATACCTCCACTTTTATGATAGCTGTTTCTTCCAAATGTT 900
| | | | |
Db 906 AAACAAATTTGATGATATACCTCCACTTTTATGATAGCTGTTTCTTCCAAATGTT 965
| | | | |
QY 901 GTCCGATATTTAAAGCACTACTATTCCTGCCATGCTGAGAAAGAACTAGGAATG 960
| | | | |
Db 966 GTCCGATATTTAAAGCACTACTATTCCTGCCATGCTGAGAAAGAACTAGGAATG 1025
| | | | |
QY 961 AGACATGTTGGGAAGACGTCAACAAATTAACAAACCTGAGATATGTTCCAGTTG 1017
| | | | |
Db 1026 AGACATGTTGGGAAGACGTCAACAAATTAACAAACCTGAGATATGTTCCAGTTG 1082
| | | | |

RESULT 6
US-10-010-667A-1
; Sequence 1, Application US/10010667A
; Patent No. 6887975
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; FILE REFERENCE: 511582001601
; CURRENT APPLICATION NUMBER: US/10/010,667A
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-010-667A-1

Query Match 100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.5e-304;

Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 241 ATGGAAGCAGAAAAGACATCAACCAAGAACTTTGGAAAATGAAAGCTTAGAGA 60
| | | | |
Db 66 ATGGAAGCAGAAAAGACATCAACCAAGAACTTTGGAAAATGAAAGCTTAGAGA 125
| | | | |
QY 61 AATTGAAAGAAAGCATTATTTGCAATGAAGACAGGAGAGACAGCATGCTTAAAGA 120
| | | | |
Db 126 AATTGAAAGAAAGCATTATTTGCAATGAAGACAGGAGAGACAGCATGCTTAAAGA 185
| | | | |
QY 121 CTTGCTTTTGGATTTGACCAACAGCCCATGCTGATGAATTTGACCTCCCTAGAA 180
| | | | |
Db 186 CTTGCTTTTGGATTTGACCAACAGCCCATGCTGATGAATTTGACCTCCCTAGAA 245
| | | | |
QY 181 CTTGAGCAGACAGGAACTTTTCCAGAGTGGCACTTGCATTTAAATAGCTGAT 240
| | | | |
Db 246 CTTGAGCAGACAGGAACTTTTCCAGAGTGGCACTTGCATTTAAATAGCTGAT 305
| | | | |
QY 241 ATAGCATCTGACATTTCTTTTACACTCTTCTGAGGAAATATTCACCTTTAGCACT 300
| | | | |
Db 306 ATAGCATCTGACATTTCTTTTACACTCTTCTGAGGAAATATTCACCTTTAGCACT 365
| | | | |
QY 301 TCCCATCAACAAATTTTATTAATTCATCTGCTGATCAACAAATCTTGGCAATG 360
| | | | |
Db 366 TCCCATCAACAAATTTTATTAATTCATCTGCTGATCAACAAATCTTGGCAATG 425
| | | | |
QY 361 GTTTCATGACTCTGTGGCATTTGTTTACCTGCCAGGATGATGACCAATTTGTC 420
| | | | |
Db 426 GTTTCATGACTCTGTGGCATTTGTTTACCTGCCAGGATGATGACCAATTTGTC 485
| | | | |
QY 421 CTTCAATATGGAACCAAGTATGAAGATTCCACATTGGTTGATTAAGATGTTAACA 480
| | | | |
Db 486 CTTCAATATGGAACCAAGTATGAAGATTCCACATTGGTTGATTAAGATGTTAACA 545
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QY 481 AGAAGACATTTGGGCTTCTCAAGTTCTTTTGGCTGATCTGATGCAATTTATAGTCTG 540
| | | | |
Db 546 AGAAGACATTTGGGCTTCTCAAGTTCTTTTGGCTGATCTGATGCAATTTATAGTCTG 605
| | | | |
QY 541 TCTTACCCATGAGGCGATCTCAGATACAGTTGCTAACTGGGCAATCAACAGTCT 600
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Db 606 TCTTACCCATGAGGCGATCTCAGATACAGTTGCTAACTGGGCAATCAACAGTCT 665
| | | | |
QY 601 CAACAAATTAAGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 660
| | | | |
Db 666 CAACAAATTAAGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 725
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QY 661 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGTGATCTTATCCATCT 720
| | | | |
Db 726 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGTTGGCTGTGATCTTATCCATCT 785
| | | | |
QY 721 GTGAGTGAATCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATGTT 780
| | | | |
Db 786 GTGAGTGAATCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATGTT 845
| | | | |
QY 781 TCCCTTCTACTGGGCAATATACAGCAATGATTTTGGCTGAAATAGTGAATGATATAT 840
| | | | |
Db 846 TCCCTTCTACTGGGCAATATACAGCAATGATTTTGGCTGAAATAGTGAATGATATAT 905
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QY 841 AAACAAATTTGATGATATACCTCCACTTTTATGATAGCTGTTTCTTCCAAATGTT 900
| | | | |
Db 906 AAACAAATTTGATGATATACCTCCACTTTTATGATAGCTGTTTCTTCCAAATGTT 965
| | | | |
QY 901 GTCCGATATTTAAAGCACTACTATTCCTGCCATGCTGAGAAAGAACTAGGAATG 960
| | | | |
Db 966 GTCCGATATTTAAAGCACTACTATTCCTGCCATGCTGAGAAAGAACTAGGAATG 1025
| | | | |
QY 961 AGACATGTTGGGAAGACGTCAACAAATTAACAAACCTGAGATATGTTCCAGTTG 1017
| | | | |
Db 1026 AGACATGTTGGGAAGACGTCAACAAATTAACAAACCTGAGATATGTTCCAGTTG 1082
| | | | |

RESULT 7
US-10-012-896-878

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Sequence 878, Application US/10012896
Patent No. 6943236
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Iasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT FILING DATE: 2001-12-10
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FaSTSeq for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-878

Query Match      100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.5e-304;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGAAGCAGAAAAGACATCAACAAACCAAGAACTTTGGAAAATGAAGCTTAGAGAGA 60
66 ATGGAAGCAGAAAAGACATCAACAAACCAAGAACTTTGGAAAATGAAGCTTAGAGAGA 125
61 AATTTAGAAAGAACGATTATTTGCTAAGACACGGGAGAGACCGCATGTCTAAAGAGA 120
126 AATTTAGAAAGAACGATTATTTGCTAAGACACGGGAGAGACCGCATGTCTAAAGAGA 185
121 CCTGTCCTTTTGCATTTGACACCAAGCCCATGCTGATGAATTTGACCTGCTCAGAA 180
186 CCTGTCCTTTTGCATTTGACACCAAGCCCATGCTGATGAATTTGACCTGCTCAGAA 245
181 CTTGACGACACACAGGAACCTTTCCACAGTGGCATTGSCCAATTAATAGTGTCTATT 240
246 CTTGACGACACACAGGAACCTTTCCACAGTGGCATTGSCCAATTAATAGTGTCTATT 305
241 ATAGCATCTCTGACTTTTCTTTTCACTCTTTGAGGGAAGTAATTCACCTTTAGCAACT 300
306 ATAGCATCTCTGACTTTTCTTTTCACTCTTTGAGGGAAGTAATTCACCTTTAGCAACT 365
301 TCCCATCAACATATTTTATTAATAATTCATCTCTGCTCATCAACAAAGCTTGGCAATG 360
366 TCCCATCAACATATTTTATTAATAATTCATCTCTGCTCATCAACAAAGCTTGGCAATG 425
361 GTTTCATCACTCTCTTGGCATGTGTTTACCTGSCAGAGTGTGTATACAGCAATTTGTCCA 420
426 GTTTCATCACTCTCTTGGCATGTGTTTACCTGSCAGAGTGTGTATACAGCAATTTGTCCA 485
421 CTTCATATATGGAACCAAGTATAGAAATTTCACATTTGTTGATAGTGAATGTTTAAACA 480
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486 CTTATATATGGAACCAAGTATAGAAATTTCACATTTGTTGATAGTGAATGTTTAAACA 545
481 AGAAGCAGTTTGGGCTTCTCAGTTTCTTTTGTGCTGACTGATGCAATTTATAGTCTG 540
546 AGAAGCAGTTTGGGCTTCTCAGTTTCTTTTGTGCTGACTGATGCAATTTATAGTCTG 605
541 TCTTACCCATGAGCGCATCTTAAGATACAAAGTTTCTTAACTGGGCAATTAACAGGTC 600
606 TCTTACCCATGAGCGCATCTTAAGATACAAAGTTTCTTAACTGGGCAATTAACAGGTC 665
601 CAACAAATTAAGAAAGATGCTGATTTGAGCATGATGTTTGAAGATGAGATTTATGTG 660
666 CAACAAATTAAGAAAGATGCTGATTTGAGCATGATGTTTGAAGATGAGATTTATGTG 725
661 TCTCTGGAATTTGTGGAATTTGGAATTAAGCTGCTGTTGCTGATGATCTTATTCATCT 720
726 TCTCTGGAATTTGTGGAATTTGGAATTAAGCTGCTGTTGCTGATGATCTTATTCATCT 785
721 GTGAGTCACTTTTGACATGAGAGAAATTTACTATATTTACAGACCAAGCTAGAAATGTT 780
786 GTGAGTCACTTTTGACATGAGAGAAATTTACTATATTTACAGACCAAGCTAGAAATGTT 845
781 TCCCTTCTACTGGGACAAATACAGCATTTGATTTTGGCTGGAATTAAGTGAATGATATA 840
846 TCCCTTCTACTGGGACAAATACAGCATTTGATTTTGGCTGGAATTAAGTGAATGATATA 905
841 AAACAAATTTGATGATATATACCTTCCAACTTTTATGATAGTGTGTTTCTTCCAAATGTT 900
906 AAACAAATTTGATGATATATACCTTCCAACTTTTATGATAGTGTGTTTCTTCCAAATGTT 965
901 GTCTGATATTTTAAAGACATCTATTTCTGCGCATGCTTGAGAAAGAAATCTGAAGATT 960
966 GTCTGATATTTTAAAGACATCTATTTCTGCGCATGCTTGAGAAAGAAATCTGAAGATT 1025
961 AGACATGTTGGGAAGACGTCACCAAAATTAACAAACCTGAGATATGTTCCAGATTG 1017
1026 AGACATGTTGGGAAGACGTCACCAAAATTAACAAACCTGAGATATGTTCCAGATTG 1082
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RESULT 8
US-09-949-016-2686
Sequence 2686, Application US/09949016
Patent No. 6812319
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT FILING DATE: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FaSTSeq for Windows Version 4.0
SEQ ID NO 2686
LENGTH: 1147
TYPE: DNA
ORGANISM: Human
US-09-949-016-2686

Query Match      99.8%; Score 1015.4; DB 3; Length 1147;
Best Local Similarity 99.9%; Pred. No. 7.8e-304;
Matches 1016; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGGAAGCAGAAAAGACATCAACAAACCAAGAACTTTGAAAATGAAGCTTAGAGAGA 60
33 ATGGAAGCAGAAAAGACATCAACAAACCAAGAACTTTGAAAATGAAGCTTAGAGAGA 92
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QY 61 AATTGAGAGAGAGATTAATTGATAGAGACAGGAGAGACAGACATGCTTAAAGA 120
DB 93 AATTGAGAGAGAGATTAATTGATAGAGACAGGAGAGACAGACATGCTTAAAGA 152
QY 121 CTTGCTTTTTCATTTTGCACCAAGCCCATGCTGATGATTTGACTGCTTCAAA 180
DB 153 CTTGCTTTTTCATTTTGCACCAAGCCCATGCTGATGATTTGACTGCTTCAAA 212
QY 181 CTTGAGACACAGAGAACTCTTTCAGAGTGGCACTTGGCAATTAATAGCTGAT 240
DB 213 CTTGAGACACAGAGAACTCTTTCAGAGTGGCACTTGGCAATTAATAGCTGAT 272
QY 241 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGAGATTAATCACTTTAGCACT 300
DB 273 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGAGATTAATCACTTTAGCACT 332
QY 301 TCCCATCAACAAATTTTAAATTTTAAATTTTCAATCTGCTGATCAACAAAGCTTGGCAATG 360
DB 333 TCCCATCAACAAATTTTAAATTTTAAATTTTCAATCTGCTGATCAACAAAGCTTGGCAATG 392
QY 361 GTTTCATCACTCTCTTGGCACTTGTTCAGTGGAGTGTGATAGAGCAATTTGTCAA 420
DB 393 GTTTCATCACTCTCTTGGCACTTGTTCAGTGGAGTGTGATAGAGCAATTTGTCAA 452
QY 421 CTTCATATAGGAAACAAGTATTAAGAACTTCAATGCTTGGATTAAGTGAATTTAACA 480
DB 453 CTTCATATAGGAAACAAGTATTAAGAACTTCAATGCTTGGATTAAGTGAATTTAACA 512
QY 481 AGAAGCACTTTGGGCTTCTCACTTTCTTTTGTCTGATCTGATGCAATTTAAGTCTG 540
DB 513 AGAAGCACTTTGGGCTTCTCACTTTCTTTTGTCTGATCTGATGCAATTTAAGTCTG 572
QY 541 TCTTACCCATGAGGAGTCTTCACTGATCAAGTGTGAACTGGGCACTTCAACAGTCT 600
DB 573 TCTTACCCATGAGGAGTCTTCACTGATCAAGTGTGAACTGGGCACTTCAACAGTCT 632
QY 601 CAACAAATTAAGAGAGTCTTGGATTAAGTGAATTTTGAAGTGAATTTAAGT 660
DB 633 CAACAAATTAAGAGAGTCTTGGATTAAGTGAATTTTGAAGTGAATTTAAGT 692
QY 661 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGCTGCTGATCTTATTTCACTCT 720
DB 693 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGCTGCTGATCTTATTTCACTCT 752
QY 721 GTGAGTGACTCTTGAATGAGAGAACTTCACTATATTGAGAGCAAGTGAATTTGTT 780
DB 753 GTGAGTGACTCTTGAATGAGAGAACTTCACTATATTGAGAGCAAGTGAATTTGTT 812
QY 781 TCCCTTCTACTGGGCAACAATACAGCATTTGTTTCTGGAATTAAGTGAATTA 840
DB 813 TCCCTTCTACTGGGCAACAATACAGCATTTGTTTCTGGAATTAAGTGAATTA 872
QY 841 AAACAAATTTGATGATTAACCTTCACTTTTATGATGCTTTTCTTCCATTTGTT 900
DB 873 AAACAAATTTGATGATTAACCTTCACTTTTATGATGCTTTTCTTCCATTTGTT 932
QY 901 GTCCGATATTTAAAGCAATTAATCTGCGCACTGCTGAGAGAAATTAAGTGAAT 960
DB 933 GTCCGATATTTAAAGCAATTAATCTGCGCACTGCTGAGAGAAATTAAGTGAAT 992
QY 961 AGACATGTTGGAGAGAGCTCAACAAATTAAGAGAGATTAAGTGAATTTGTT 1017
DB 993 AGACATGTTGGAGAGAGAGCTCAACAAATTAAGAGAGATTAAGTGAATTTGTT 1049

RESULT 9
US-09-323-873A-6
Sequence 6, Application US/09323873A

Patent No. 6329503
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong

APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
FILE REFERENCE: 129.16US02
CURRENT APPLICATION NUMBER: US/09/323,873A
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 3627
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-323-873A-6

Query Match 74.8%; Score 760.6; DB 3; Length 3627;
Best Local Similarity 99.5%; Pred. No. 1.2e-224;
Matches 763; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGGAAGAGAGAGAGATTAATTTGATAGAGACAGGAGAGACAGACATGCTTAAAGA 60
DB 96 ATGGAAGAGAGAGAGATTAATTTGATAGAGACAGGAGAGACAGACATGCTTAAAGA 155
QY 61 AATTGAGAGAGAGATTAATTGATAGAGACAGGAGAGACAGACATGCTTAAAGA 120
DB 156 AATTGAGAGAGAGATTAATTGATAGAGACAGGAGAGACAGACATGCTTAAAGA 215
QY 121 CTTGCTTTTTCATTTTGCACCAAGCCCATGCTGATGATTTGACTGCTTCAAA 180
DB 216 CTTGCTTTTTCATTTTGCACCAAGCCCATGCTGATGATTTGACTGCTTCAAA 275
QY 216 CTTGCTTTTTCATTTTGCACCAAGCCCATGCTGATGATTTGACTGCTTCAAA 275
DB 216 CTTGCTTTTTCATTTTGCACCAAGCCCATGCTGATGATTTGACTGCTTCAAA 275
QY 241 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGAGATTAATCACTTTAGCACT 300
DB 336 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGAGATTAATCACTTTAGCACT 395
QY 301 TCCCATCAACAAATTTTAAATTTTCAATCTGCTGATCAACAAAGCTTGGCAATG 360
DB 396 TCCCATCAACAAATTTTAAATTTTCAATCTGCTGATCAACAAAGCTTGGCAATG 455
QY 361 GTTTCATCACTCTTGGCACTTGTTCAGTGGAGTGTGATAGAGCAATTTGTCAA 420
DB 456 GTTTCATCACTCTTGGCACTTGTTCAGTGGAGTGTGATAGAGCAATTTGTCAA 515
QY 421 CTTCATATAGGAAACAAGTATTAAGAACTTCACTTGTGATTAAGTGAATTTAACA 480
DB 516 CTTCATATAGGAAACAAGTATTAAGAACTTCACTTGTGATTAAGTGAATTTAACA 575
QY 481 AGAAGCACTTTGGGCTTCTCACTTTCTTTTGTGCTGATCTGATGCAATTTAAGTCTG 540
DB 576 AGAAGCACTTTGGGCTTCTCACTTTCTTTTGTGCTGATCTGATGCAATTTAAGTCTG 635
QY 541 TCTTACCCATGAGGAGATCTTCACTGATTAAGTGTCTTAACTGGGCAATTAACAGTCT 600
DB 636 TCTTACCCATGAGGAGATCTTCACTGATTAAGTGTCTTAACTGGGCAATTAACAGTCT 695
QY 601 CAACAAATTAAGAGAGTCTGATTAAGAACTTCACTTGTGATTAAGTGAATTTAAGT 660
DB 696 CAACAAATTAAGAGAGTCTGATTAAGAACTTCACTTGTGATTAAGTGAATTTAAGT 755
QY 661 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGCTGCTGATCTTATTTCACTCT 720
DB 756 TCTCTGGGAATTTGGGATTTGGCAATCTGCTCTGCTGCTGATCTTATTTCACTCT 815
QY 721 GTGAGTGACTCTTGAATGAGAGAACTTCACTATATTGAGAGCA 767


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Db      816 GTGAGTGAAGCTTTGACATGAGAGAAATTCATATTCAGGTAA 862

RESULT 10
US-09-455-486-4
; Sequence 4, Application US/09455486
; Patent No. 6833438
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.17-US-11
; CURRENT APPLICATION NUMBER: US/09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-455-486-4

Query Match      74.8%; Score 760.6; DB 3; Length 3627;
Best Local Similarity 99.5%; Pred. No. 1.2e-224;
Matches 763; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 ATGGAAGAGAGAAAGACATCAACCAAGAACTTTGGAAATGAAGCTTAGAGA 60
Db      96 ATGGAAGAGAGAAAGACATCAACCAAGAACTTTGGAAATGAAGCTTAGAGA 155
QY      61 AATTTAGAAGAGACGATTAATTTGCAATAGACACGGAGAGACAGCATGCTAAAAA 120
Db      156 AATTTAGAAGAGACGATTAATTTGCAATAGACACGGAGAGACAGCATGCTAAAAA 215
QY      121 CCTGTCCTTTTGATTTGACCAACAGCCCATGCTGAATTTTACCTGCCCTTAGAA 180
Db      216 CCTGTCCTTTTGATTTGACCAACAGCCCATGCTGAATTTTACCTGCCCTTAGAA 275
QY      181 CTTGAGCACAACAGGAACCTTTTCCAGTGGCACTTGCCCAATTAATAGCTGTATT 240
Db      276 CTTGAGCACAACAGGAACCTTTTCCAGTGGCACTTGCCCAATTAATAGCTGTATT 335
QY      301 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGAAATTAATCAACCTTTAGCACT 300
Db      336 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGAAATTAATCAACCTTTAGCACT 395
QY      301 TCCCATCAACATATTTTATATAAATTTCCAAATCTGTCTATCAACAAAGCTTGGCAATG 360
Db      396 TCCCATCAACATATTTTATATAAATTTCCAAATCTGTCTATCAACAAAGCTTGGCAATG 455
QY      361 GTTTCATCACTCTTTGGCATTTGTTTACCTGCAAGTGTATGATAGACAGCAATTTGCCAA 420
Db      456 GTTTCATCACTCTTTGGCATTTGTTTACCTGCAAGTGTATGATAGACAGCAATTTGCCAA 515
QY      421 CTTCATATATGAAACCAAGTATTAAGAGTTTCCACATTTGGTGAATAAGGATGTTAACA 480
Db      516 CTTCATATATGAAACCAAGTATTAAGAGTTTCCACATTTGGTGAATAAGGATGTTAACA 575
QY      481 AGAAGCAAGTTTGGGCTTCTCAAGTTTCTTTTGGCTGTACTGCATGCAATTTTATAGCTG 540
Db      576 AGAAGCAAGTTTGGGCTTCTCAAGTTTCTTTTGGCTGTACTGCATGCAATTTTATAGCTG 635
QY      541 TCTTACCCCAATGAGGAGATCTTACAGATACAGTGTATTAATGCGGCAATCAACAGGTC 600
Db      636 TCTTACCCCAATGAGGAGATCTTACAGATACAGTGTATTAATGCGGCAATCAACAGGTC 655
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QY      601 CAACAAATATAAGAGATGCTTGATTTGAGCATGATTTGGAAATGAGATTTATGTG 660
Db      696 CAACAAATATAAGAGATGCTTGATTTGAGCATGATTTGGAAATGAGATTTATGTG 755
QY      661 TCTGAGGAATTTGGGATTTGGCAATCTGAGCTGTTGGCTGTGACATCTTATTCATCT 720
Db      756 TCTGAGGAATTTGGGATTTGGCAATCTGAGCTGTTGGCTGTGACATCTTATTCATCT 815
QY      721 GTGAGTGAAGCTTTGACATGAGAGAAATTCATATTCAGAGCAA 767
Db      816 GTGAGTGAAGCTTTGACATGAGAGAAATTCATATTCAGGTAA 862

RESULT 11
US-10-010-667A-6
; Sequence 6, Application US/10010667A
; Patent No. 6887975
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 511582001601
; CURRENT APPLICATION NUMBER: US/10/010,667A
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-667A-6

Query Match      74.8%; Score 760.6; DB 3; Length 3627;
Best Local Similarity 99.5%; Pred. No. 1.2e-224;
Matches 763; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 ATGGAAGAGAGAAAGACATCAACCAAGAACTTTGGAAATGAAGCTTAGAGA 60
Db      96 ATGGAAGAGAGAAAGACATCAACCAAGAACTTTGGAAATGAAGCTTAGAGA 155
QY      61 AATTTAGAAGAGACGATTAATTTGCAATAGACACGGAGAGACAGCATGCTAAAAA 120
Db      156 AATTTAGAAGAGACGATTAATTTGCAATAGACACGGAGAGACAGCATGCTAAAAA 215
QY      121 CCTGTCCTTTTGATTTGACCAACAGCCCATGCTGAATTTTACCTGCCCTTAGAA 180
Db      216 CCTGTCCTTTTGATTTGACCAACAGCCCATGCTGAATTTTACCTGCCCTTAGAA 275
QY      181 CTTGAGCACAACAGGAACCTTTTCCAGTGGCACTTGCCCAATTAATAGCTGTATT 240
Db      276 CTTGAGCACAACAGGAACCTTTTCCAGTGGCACTTGCCCAATTAATAGCTGTATT 335
QY      241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGAAATTAATCAACCTTTAGCACT 300
Db      336 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGAAATTAATCAACCTTTAGCACT 395
QY      301 TCCCATCAACATATTTTATATAAATTTCCAAATCTGTCTATCAACAAAGCTTGGCAATG 360
Db      396 TCCCATCAACATATTTTATATAAATTTCCAAATCTGTCTATCAACAAAGCTTGGCAATG 455
QY      361 GTTTCATCACTCTTTGGCATTTGTTTACCTGCAAGTGTATGATAGACAGCAATTTGCCAA 420
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Db 456 GTTTCATCACTCTCTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCGA 515
Qy 421 CTTCAATATGGAACCAAGTATATAGAAAGTTTCCACATTTGGTGAATGATGTTTACA 480
Db 516 CTTCAATATGGAACCAAGTATATAGAAAGTTTCCACATTTGGTGAATGATGTTTACA 575
Qy 481 AGAAGCAGTTGGGCTTCTCAGTTTCTTTTCTGCTACTGATGCAATTAATAGCTG 540
Db 576 AGAAGCAGTTGGGCTTCTCAGTTTCTTTTCTGCTACTGATGCAATTAATAGCTG 635
Qy 541 TCTTACCCATAGAGCCATCTTACAGATACAAAGTTGCTTAACTGGGCAATCAACAGCTC 600
Db 636 TCTTACCCATAGAGCCATCTTACAGATACAAAGTTGCTTAACTGGGCAATCAACAGCTC 695
Qy 601 CAACAAATTAAGAAAGTCCCTGATGATGATGTTTGGAGATAGAGATTTATGTC 660
Db 696 CAACAAATTAAGAAAGTCCCTGATGATGATGTTTGGAGATAGAGATTTATGTC 755
Qy 661 TCTTGGGAATTTGGGATTTGGCAATCTGGCTCTGGCTGTGATCATCTTATTCATCT 720
Db 756 TCTTGGGAATTTGGGATTTGGCAATCTGGCTCTGGCTGTGATCATCTTATTCATCT 815
Qy 721 GTGAGTACTCTTGTGACATGAGAGAAATTCATATATTCAGAGCA 767
Db 816 GTGAGTACTCTTGTGACATGAGAGAAATTCATATATTCAGAGCA 862

RESULT 12

US-09-439-313-342/c
Sequence 342, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solik, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439.313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-342

Query Match 50.7%; Score 516; DB 3; Length 592;

Best Local Similarity 99.6%; Pred. No. 2.4e-149;

Matches 516; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGGAAGCAGAAAGACATCACAAACCAAGAACTTTGAAAAATGAAGCTTAGAGA 60
Db 518 ATGGAAGCAGAAAGACATCACAAACCAAGAACTTTGAAAAATGAAGCTTAGAGA 459
Qy 61 AATTGGAAGAAAGCATTTTTCATAGAGACACGGAGAGACACGATGCTTAAAGA 120
Db 458 AATTGGAAGAAAGCATTTTTCATAGAGACACGGAGAGACACGATGCTTAAAGA 399
Qy 121 CCTGTGCTTTTGCATTTGACCAACAGCCCATGATGAATTTAGTCCCTTAGA 180
Db 398 CCTGTGCTTTTGCATTTGACCAACAGCCCATGATGAATTTAGTCCCTTAGA 339
Qy 181 CTTGACACACACAGAACTTTTCCACAGTGGCACTTGGCAATTAATAGCTGTATT 240

Db 338 CTTGACACACACAGAACTTTTCCACAGTGGCACTTGGCAATTAATAGCTGTATT 279
Qy 241 ATGACATCTGACTTTTCTTACACTCTTCTGAGGAAATTAATCACTTTAGCACT 300
Db 278 ATGACATCTGACTTTTCTTACACTCTTCTGAGGAAATTAATCACTTTAGCACT 219
Qy 301 TCCCATCAACATATTTTATTAATTCGAATCTGGTCAATCAACAAAGCTTGGCAATG 360
Db 218 TCCCATCAACATATTTTATTAATTCGAATCTGGTCAATCAACAAAGCTTGGCAATG 159
Qy 361 GTTTCATCACTCTCTTGGCATTGTTTACCTGCAAGTGTGATAGCAGCAATGTCGA 420
Db 158 GTTTCATCACTCTCTTGGCATTGTTTACCTGCAAGTGTGATAGCAGCAATGTCGA 99
Qy 421 CTTCAATATGGAACCAAGTATATAGAAAGTTTCCACATTTGGTGAATAGGATTTACA 480
Db 98 CTTCAATATGGAACCAAGTATATAGAAAGTTTCCACATTTGGTGAATAGGATTTACA 39
Qy 481 AGAAGCAGTTGGGCTTCTCAGTTTCTTTTGTGCTGT 518
Db 38 AGAAGCAGTTGGGCTTCTCAGTTTCTTTTGTGCTGT 1

RESULT 13

US-09-352-616A-342/c
Sequence 342, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352.616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-342

Query Match 50.7%; Score 516; DB 3; Length 592;

Best Local Similarity 99.6%; Pred. No. 2.4e-149;

Matches 516; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGGAAGCAGAAAGACATCACAAACCAAGAACTTTGAAAAATGAAGCTTAGAGA 60
Db 518 ATGGAAGCAGAAAGACATCACAAACCAAGAACTTTGAAAAATGAAGCTTAGAGA 459
Qy 61 AATTGGAAGAAAGCATTTTTCATAGAGACACGGAGAGACACGATGCTTAAAGA 120
Db 458 AATTGGAAGAAAGCATTTTTCATAGAGACACGGAGAGACACGATGCTTAAAGA 399
Qy 121 CCTGTGCTTTTGCATTTGACCAACAGCCCATGATGAATTTAGTCCCTTAGA 180
Db 398 CCTGTGCTTTTGCATTTGACCAACAGCCCATGATGAATTTAGTCCCTTAGA 339
Qy 181 CTTGACACACACAGAACTTTTCCACAGTGGCACTTGGCAATTAATAGCTGTATT 240
Db 338 CTTGACACACACAGAACTTTTCCACAGTGGCACTTGGCAATTAATAGCTGTATT 279
Qy 241 ATGACATCTGACTTTTCTTACACTCTTCTGAGGAAATTAATCACTTTAGCACT 300
Db 278 ATGACATCTGACTTTTCTTACACTCTTCTGAGGAAATTAATCACTTTAGCACT 219
Qy 301 TCCCATCAACATATTTTATTAATTCGAATCTGGTCAATCAACAAAGCTTGGCAATG 360

Db 218 TCCCATCAACAATATTTTATTAATAATTCCAATCTGTGATCAACAAGTCTTGCAATG 159
OY 361 GTTTCATCACTCTCTTGAGCATTTGATTACCTGCCAGGTGTGATGACGAAATTTGCCAA 420
Db 158 GTTTCATCACTCTCTTGAGCATTTGATTACCTGCCAGGTGTGATGACGAAATTTGCCAA 99
OY 421 CTTCAATATGGAACCAAGTATTAAGAAGTTTCCACATTTGGTGTGATTAAGTGTATTAACA 480
Db 98 CTTCAATATGGAACCAAGTATTAAGAAGTTTCCACATTTGGTGTGATTAAGTGTATTAACA 39
OY 481 AGAAGCAGTTGGGCTTCTCAGTTTCTTTTGGCTGT 518
Db 38 AGAAGCAGATTGGGCTTCTCAGTTTCTTTTGGCTGT 1

RESULT 14

US-09-636-215-342/C
/ Sequence 342, Application US/09636215
/ Patent No. 6620922
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqi
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darriek
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.42717C17
/ CURRENT APPLICATION NUMBER: US/09/636,215
/ CURRENT FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 852
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 342
/ LENGTH: 592
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-636-215-342

Query Match 50.7%; Score 516; DB 3; Length 592;
Best Local Similarity 99.6%; Pred. No. 2.4e-149;
Matches 516; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ATGGAAGCAGAAAGACATCAACAACCAAGAACTTTGAAAATGAAGCTTAGAGA 60
Db 518 ATGGAAGCAGAAAGACATCAACAACCAAGAACTTTGAAAATGAAGCTTAGAGA 459
OY 61 AATTTGAAGAAGACATTAATTTGCAATAGGACAGGGAGACGACATGCTAAAGA 120
Db 458 AATTTGAAGAAGACATTAATTTGCAATAGGACAGGGAGACGACATGCTAAAGA 399
OY 121 CCGTGTCTTTTGATTTGACCAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGA 180
Db 398 CCGTGTCTTTTGATTTGACCAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGA 339
OY 181 CTTGACACACACAGAACTCTTTTCCACAGTGGCACTTGCCAAATTAATAGTCTGAT 240
Db 338 CTTGACACACACAGAACTCTTTTCCACAGTGGCACTTGCCAAATTAATAGTCTGAT 279
OY 241 ATAGCATCTCTGACTTTTCTTAACCTCTGAGGGAAGTAAATTAACCTTTAGCACT 300
Db 278 ATAGCATCTCTGACTTTTCTTAACCTCTGAGGGAAGTAAATTAACCTTTAGCACT 219

OY 301 TCCCATCAACAATATTTTATTAATAATTCCAATCTGTGATCAACAAGTCTTGCAATG 360
Db 218 TCCCATCAACAATATTTTATTAATAATTCCAATCTGTGATCAACAAGTCTTGCAATG 159
OY 361 GTTTCATCACTCTCTTGAGCATTTGATTACCTGCCAGGTGTGATGACGAAATTTGCCAA 420
Db 158 GTTTCATCACTCTCTTGAGCATTTGATTACCTGCCAGGTGTGATGACGAAATTTGCCAA 99
OY 421 CTTCAATATGGAACCAAGTATTAAGAAGTTTCCACATTTGGTGTGATTAAGTGTATTAACA 480
Db 98 CTTCAATATGGAACCAAGTATTAAGAAGTTTCCACATTTGGTGTGATTAAGTGTATTAACA 39
OY 481 AGAAGCAGTTGGGCTTCTCAGTTTCTTTTGGCTGT 518
Db 38 AGAAGCAGATTGGGCTTCTCAGTTTCTTTTGGCTGT 1

RESULT 15

US-09-685-166A-342/C
/ Sequence 342, Application US/09685166A
/ Patent No. 6630305
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqi
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darriek
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.427C21
/ CURRENT APPLICATION NUMBER: US/09/685,166A
/ CURRENT FILING DATE: 2000-10-10
/ NUMBER OF SEQ ID NOS: 898
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 342
/ LENGTH: 592
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-685-166A-342

Query Match 50.7%; Score 516; DB 3; Length 592;
Best Local Similarity 99.6%; Pred. No. 2.4e-149;
Matches 516; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ATGGAAGCAGAAAGACATCAACAACCAAGAACTTTGAAAATGAAGCTTAGAGA 60
Db 518 ATGGAAGCAGAAAGACATCAACAACCAAGAACTTTGAAAATGAAGCTTAGAGA 459
OY 61 AATTTGAAGAAGACATTAATTTGCAATAGGACAGGGAGACGACATGCTAAAGA 120
Db 458 AATTTGAAGAAGACATTAATTTGCAATAGGACAGGGAGACGACATGCTAAAGA 399
OY 121 CCGTGTCTTTTGATTTGACCAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGA 180
Db 398 CCGTGTCTTTTGATTTGACCAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGA 339
OY 181 CTTGACACACACAGAACTCTTTTCCACAGTGGCACTTGCCAAATTAATAGTCTGAT 240
Db 338 CTTGACACACACAGAACTCTTTTCCACAGTGGCACTTGCCAAATTAATAGTCTGAT 279

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Qy 241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACT 300
Db 278 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACT 219
Qy 301 TCCCATCAACAATTTTAAATTCCAATCTGTGTCATCAACAAGTCTTGCCAAATG 360
Db 218 TCCCATCAACAATTTTAAATTCCAATCTGTGTCATCAACAAGTCTTGCCAAATG 159
Qy 361 GTTTCATCACTCTCTTGCAATGTTTACCTGCAAGTGTGATAGCAGCAATTTGCCAA 420
Db 158 GTTTCATCACTCTCTTGCAATGTTTACCTGCAAGTGTGATAGCAGCAATTTGCCAA 99
Qy 421 CTTCAATATGGAACCAAGTATTAAGAAAGTTTCCACATTTGTTGATTAAGTATTTACA 480
Db 98 CTTCAATATGGAACCAAGTATTAAGAAAGTTTCCACATTTGTTGATTAAGTATTTACA 39
Qy 481 AGAAGCAGTTGGGCTTCTCAGTTTCTTTTGGCTGT 518
Db 38 AGAAGCAGTTGGGCTTCTCAGTTTCTTTTGGCTGT 1

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OM nucleic - nucleic search, using sw model

Run on: December 4, 2005, 20:13:31 / Search time 682.751 Seconds
(without alignments)
9927.475 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 333346308 residues

Total number of hits satisfying chosen parameters: 9993994

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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2: geneseqn1990s: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1017	100.0	1193	8	ACD02597 cDNA enco
5	1017	100.0	1193	14	ADY92658 Human STR
6	1017	100.0	1195	4	AAH93924 P789P full
7	1017	100.0	1195	4	AAH93924 Human pro
8	1017	100.0	1195	5	ACA59968 Prostate
9	1017	100.0	1195	6	AB195531 Human P78
10	1017	100.0	1195	6	ABK92128 Prostate
11	1017	100.0	1195	8	ACC95695 Prostate
12	1017	100.0	1195	10	ADB75572 Prostate
13	1017	100.0	1195	10	ADB14328 Human pro
14	1017	100.0	1195	10	AD63162 Human STR
15	1017	100.0	1195	10	AD62763 Human STR
16	1017	100.0	1195	10	ADG26744 Human pro
17	1017	100.0	1195	11	ADN39812 Cancer/an
18	1017	100.0	1195	11	ADN39395 Cancer/an
19	1017	100.0	1195	11	ADP88258 Prostate

20	1017	100.0	1195	12	ADL06462 Human tum
21	1017	100.0	1195	12	ADL06436 Human tum
22	1017	100.0	1195	12	ADJ75176 Marker ge
23	1017	100.0	1201	13	ADX33625 Plant full
24	1017	100.0	1277	5	ADL46020 Human ova
25	1017	100.0	1294	4	AAK51978 Human pol
26	1017	100.0	1330	13	ADRI4190 Human NF-
27	1017	100.0	1330	13	ADU06030 Novel bro
28	1017	100.0	1330	14	ADY15575 DNA encod
29	1017	100.0	1330	14	ADY19959 DNA encod
30	1004.4	98.8	1229	4	AAK52962 Human pol
31	1004	98.7	1198	8	ACD02628 STEAP-1 v
32	1002.4	98.6	1198	8	ACD02629 STEAP-1 v
33	988	97.1	1354	12	ADQ22300 Human bof
34	870	85.5	1365	8	ACD02599 cDNA enco
35	870	85.5	1365	8	ACD02630 STEAP-1 v
36	866	85.2	1369	8	ACD02632 STEAP-1 v
37	864.4	85.0	1369	8	ACD02631 STEAP-1 v
38	762.2	74.9	3627	8	ACD02601 cDNA enco
39	760.6	74.8	3627	3	AAZ49396 Human STR
40	760.6	74.8	3627	5	AAZ49396 Human STR
41	760.6	74.8	3627	8	ACD02613 cDNA enco
42	760.6	74.8	3627	8	ACD02605 cDNA enco
43	760.6	74.8	3627	8	ACD02606 cDNA enco
44	760.6	74.8	3627	8	ACD02598 cDNA enco
45	760.6	74.8	3627	8	ACD02612 cDNA enco

ALIGNMENTS

RESULT 1	ADV73174	standard; DNA; 1177 BP.
ID	ADV73174	
XX	ADV73174:	
XX	AC	ADV73174:
XX	DT	10-MAR-2005 (first entry)
XX	DE	Human colon tumor cell upregulated gene SEQ ID NO 15.
XX	KW	de; gene; cancer; neoplasm; cytostatic.
XX	OS	Homo sapiens.
XX	PN	W02004110345-A2.
XX	PD	23-DEC-2004.
XX	PF	28-OCT-2003; 2003MO-US034019.
XX	PR	29-OCT-2002; 2002US-0422176P.
XX	PA	(PHAA) PHARMACIA CORP.
XX	PI	Bourner MJ, Bu JU, Head RD, Hippenmeyer PJ, Klein BK;
XX	PI	Mezzarella RA, Staten NR;
XX	DR	WPI, 2005-03958/04.
XX	DR	P-PSDB; ADV73212.
XX	PT	New antibody that immunospecifically binds to p-cadherin, useful in
XX	PT	preparing a composition for treating or preventing a cancer-associated
XX	PT	disorder.
XX	PS	Disclosure, SEQ ID NO 15; 257pp; English.
XX	CC	The invention relates to an antibody immunospecifically binds to p-
XX	CC	cadherin or its fragment. The antibody is useful in preparing a
XX	CC	composition for treating or preventing a cancer-associated disorder. The
XX	CC	present sequence represents a gene upregulated in human colon cancer
XX	CC	cells.

SO Sequence 1177 BP; 364 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1017; DB 14; Length 1177;
Best Local Similarity 100.0%; Pred. No. 2,6e-276;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGAAGGCGAAGGATCATCAACCAAGAGAACTTTGGAAAATGAAAGCTTAGAGA 60
DB 66 ATGGAAGGCGAAGGATCATCAACCAAGAGAACTTTGGAAAATGAAAGCTTAGAGA 125
QY 61 AATTTAGAGAAGCGATTTTTCATPAGACACGGGAGAGACCAGCATGCTTAAAGA 120
DB 126 AATTTAGAGAAGCGATTTTTCATPAGACACGGGAGAGACCAGCATGCTTAAAGA 185
QY 121 CCGTGTCTTTTGGATTTGACCAAAACGCCATGCTGATGAATTTGACTGCCCTTCGAA 180
DB 186 CCGTGTCTTTTGGATTTGACCAAAACGCCATGCTGATGAATTTGACTGCCCTTCGAA 245
QY 181 CTTGAGACACACAGGAACCTTTTCCAGAGTGGCACTTGCCTAAATTAATAGCTGAT 240
DB 246 CTTGAGACACACAGGAACCTTTTCCAGAGTGGCACTTGCCTAAATTAATAGCTGAT 305
QY 241 ATAGCATCTGCACTTTTCTTTTCACTCTCTGAGGGAGTAATTCACCCCTTAGCACT 300
DB 306 ATAGCATCTGCACTTTTCTTTTCACTCTCTGAGGGAGTAATTCACCCCTTAGCACT 365
QY 301 TCCCATCAACCAATATTTTATAAAATTCCAATCTGCTGATCAACAAAGCTTGGCAAT 360
DB 366 TCCCATCAACCAATATTTTATAAAATTCCAATCTGCTGATCAACAAAGCTTGGCAAT 425
QY 361 GTTTCATCACTCTCTTGGGATGTTTACCTGCGAGGTGTATPAGACGAATTTGCCAA 420
DB 426 GTTTCATCACTCTCTTGGGATGTTTACCTGCGAGGTGTATPAGACGAATTTGCCAA 485
QY 421 CTTCAATATGGAACCAAGTATTAAGAAAGTTTCCACATTTGGTGAATTAAGATTTAA 480
DB 486 CTTCAATATGGAACCAAGTATTAAGAAAGTTTCCACATTTGGTGAATTAAGATTTAA 545
QY 481 AGAAGACAGTTGGGGCTTCTCAGTTTCTTTTGTCTGATCTGATGCAATTTTATGCTG 540
DB 546 AGAAGACAGTTGGGGCTTCTCAGTTTCTTTTGTCTGATCTGATGCAATTTTATGCTG 605
QY 541 TCTTACCACATGAGGGATCTTCAATACAGTACAGTTGCTAAACGGGCATATCAACGGTC 600
DB 606 TCTTACCACATGAGGGATCTTCAATACAGTACAGTTGCTAAACGGGCATATCAACGGTC 665
QY 601 CAACAAATTAAGAAGATGCTGATTTGAGCATGATTTGGAGAAATGAGATTTATGTC 660
DB 666 CAACAAATTAAGAAGATGCTGATTTGAGCATGATTTGGAGAAATGAGATTTATGTC 725
QY 661 TCTTGGGAATTTGGGAATTTGGCAATGCTGCTGTGTGGCTGTGACATCTATTTCCATCT 720
DB 726 TCTTGGGAATTTGGGAATTTGGCAATGCTGCTGTGTGGCTGTGACATCTATTTCCATCT 785
QY 721 GTGAGTGAATCTTTTGCATGAGAGAAATTTCACTATATTCAGAGCAAGCTTAGAATTTGT 780
DB 786 GTGAGTGAATCTTTTGCATGAGAGAAATTTCACTATATTCAGAGCAAGCTTAGAATTTGT 845
QY 781 TCCCTTCTACTGGGCAATATACAGCATTTGATTTTGGCCGTGAAATTAAGTATGATATA 840
DB 846 TCCCTTCTACTGGGCAATATACAGCATTTGATTTTGGCCGTGAAATTAAGTATGATATA 905
QY 841 AAACAAATTTGTATGTATACACCTCCAACTTTTATGATAGCTGTTTCTTCCAAATTTGT 900
DB 906 AAACAAATTTGTATGTATACACCTCCAACTTTTATGATAGCTGTTTCTTCCAAATTTGT 965
QY 901 GTTCGTATATTTTAAAGCATATCTATCTCTGCCATGCTTTAGAGAAAGATPACTGAAGATT 960
DB 966 GTTCGTATATTTTAAAGCATATCTATCTCTGCCATGCTTTAGAGAAAGATPACTGAAGATT 1025
QY 961 AGACATGTTGGGAAGACGTACCAAAATTAACAAATTAAGATGTTCCCAAGTTG 1017
DB 1026 AGACATGTTGGGAAGACGTACCAAAATTAACAAATTAAGATGTTCCCAAGTTG 1082

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RESULT 2
AA249395
ID AA249395 standard; cDNA; 1193 BP.
XX
AC AA249395;
XX
DT 14-MAR-2000 (first entry)
XX
DE Human STRAP-1 cDNA.
XX
KW Serpentine transmembrane antigen of the prostate; STRAP-1; prostate;
KW transmembrane domain; type IIIa membrane protein; expression; cancer;
KW prostate cancer; bladder cancer; colon cancer; pancreatic cancer;
KW ovarian cancer; tumour antigen; immunisation; immune response; cellular;
KW humoral; anticancer vaccine; antibody detection; diagnosis; prognosis;
KW monitoring; susceptibility; therapeutic inhibitor; drug targeting;
KW recombinant protein; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 64..1083
FT /tag= a
FT /product= "Human STRAP-1 (serpentine transmembrane
FT antigen of the prostate)"
PN MO9962941-A2.
XX
PD 09-DEC-1999.
XX
PF 01-JUN-1999; 99MO-US012157.
XX
PR 01-JUN-1998; 98US-0087520P.
PR 30-JUN-1998; 98US-0091183P.
XX
PA (UROC-) UROGENESYS INC.
PA (AFAR/) AFAR D E.
PA (HUBE/) HUBERT R S.
PA (LEON/) LEONG K.
PA (RAIT/) RAITANO A B.
PA (SAFE/) SAFFRAN D C.
XX
PI Afar DE, Hubert RS, Leong K, Raitano AB, Safran DC;
DR WPI: 2000-072832/06.
DR P-PSDB; AAY58194.
XX
PT Novel proteins useful as diagnostic markers and therapeutic targets,
PT particularly for prostatic cancer.
XX
PS Claim 4; Fig 1A; 83pp; English.
XX

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This sequence represents cDNA encoding a novel human protein, STRAP-1 (serpentine transmembrane antigen of the prostate). STRAP-1 is the prototype member of the STRAP family of proteins (AAY58194-Y58197) which exhibit a high degree of structural conservation, but which show no significant structural homology to known human proteins. The STRAP-1 gene has been localised to chromosome 7p22. STRAP-1 is thought to be a type IIIa membrane protein and is expressed predominantly in prostate cells in normal human tissues. Structurally, STRAP-1 is a 319 amino acid protein characterised by six transmembrane domains and intracellular N- and C-termini, suggesting that it folds in a "serpentine" manner into three extracellular and two intracellular loops. STRAP-1 mRNA and protein expression is maintained at high levels and throughout all stages of prostate cancer. STRAP-1 mRNA and/or protein is also overexpressed in certain other cancers, including bladder, colon, pancreatic and ovarian cancer. The function of the STRAP proteins is not known. They may be ion channels (from the presence of six transmembrane domains, a feature which is shared by certain ion channels) or gap-junction proteins (from immunohistochemical staining). STRAP-1 and STRAP-2 are cell-surface tumour antigens. Immunisation with a STRAP protein induces cellular and

CC humoral immune responses against STRAP-expressing cells. STRAP proteins
CC may be used to identify specific-binding agents, to produce anticancer
CC vaccines and to generate specific antibodies. The antibodies may be used
CC for detection, prognosis, and monitoring of cancers (or susceptibility to
CC cancer), as therapeutic inhibitors or to target therapeutic agents to
CC their site of action. STRAP nucleic acids may be used for recombinant
CC protein production, as diagnostic and prognostic reagents, for
CC identifying STRAP-expressing cells for screening inhibitors of STRAP
CC expression and for therapeutic modulation/inhibition of STRAP expression.
CC Since high levels of STRAP proteins are exposed on the cell surface, they
CC are easily targeted by systemically administered agents, and because
CC they are expressed mainly on prostatic epithelial cells, agents targeted
CC to them should have minimal side effects on other tissues
XX

SQ Sequence 1193 BP; 382 A; 219 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1017; DB 3; Length 1193;

Best Local Similarity 100.0%; Pred. No. 2,66-276;

Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGAAGACGAAAGACATCAACAACCAAGAACTTTGGAAATGAAGCTTAGAGA 60
DB 64 ATGGAAGACGAAAGACATCAACAACCAAGAACTTTGGAAATGAAGCTTAGAGA 123
QY 61 AATTAGAGAGACGATTATTTCATAGAGACGAGAGAGACAGCATGCTAAGAGA 120
DB 124 AATTAGAGAGACGATTATTTCATAGAGACGAGAGAGACAGCATGCTAAGAGA 183
QY 121 CTTGTGCTTTTGCACTTTTGCACTTTTGCACTTTTGCACTTTTGCACTTTTGCA 180
DB 184 CTTGTGCTTTTGCACTTTTGCACTTTTGCACTTTTGCACTTTTGCACTTTTGCA 243
QY 181 CTTGAGACACACAGCAAGCTTTTCCACAGTGGACATTTGCAATTAATAGTGTCTATT 240
DB 244 CTTGAGACACACAGCAAGCTTTTCCACAGTGGACATTTGCAATTAATAGTGTCTATT 303
QY 241 ATAGCATCTGCACTTTTCTTACACTTTTCTGAGGAGATTAATCACTTTAGCACT 300
DB 304 ATAGCATCTGCACTTTTCTTACACTTTTCTGAGGAGATTAATCACTTTAGCACT 363
QY 301 TCCCATCAACATATTTTATTAATTAATTCATCTCTGTCATCAACAAAGTCTTGCAATG 360
DB 364 TCCCATCAACATATTTTATTAATTAATTCATCTCTGTCATCAACAAAGTCTTGCAATG 423
QY 361 GTTTCATCACTCTCTGAGCTTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 420
DB 424 GTTTCATCACTCTCTGAGCTTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 483
QY 421 CTTCATATATGGAACCAAGTATTAAGAGTTTCCACATTTGTTGATTAAGTATTAACA 480
DB 484 CTTCATATATGGAACCAAGTATTAAGAGTTTCCACATTTGTTGATTAAGTATTAACA 543
QY 481 AGAAGACAGTTGGGCTTTCTGAGTTTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 544 AGAAGACAGTTGGGCTTTCTGAGTTTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 603
QY 541 TCTTAACCATGAGGCGATCTCTAAGATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 604 TCTTAACCATGAGGCGATCTCTAAGATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 663
QY 601 CAACAAATTAAGAGATGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 660
DB 664 CAACAAATTAAGAGATGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 723
QY 661 TCTTGGGAATTTGGGATTTGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 724 TCTTGGGAATTTGGGATTTGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
QY 721 GTGAGTACTCTTTGAGATGAGAGATTTTCACTATATTTGAGACCAAGCTAGAGATTTGTT 780
DB 784 GTGAGTACTCTTTGAGATGAGAGATTTTCACTATATTTGAGACCAAGCTAGAGATTTGTT 843
QY 781 TCCCTTCTACTGGGACAAATACAGCATGTATTTTCTGGAATTAAGTGTAGATATA 840

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DB 844 TCCCTTCTACTGGGACAAATACAGCATGTATTTTCTGGAATTAAGTGTAGATATA 903
QY 841 AAACAATTTGATGATATACCTCCAACTTTATGATAGTGTGCTTCCAAATGTT 900
DB 904 AAACAATTTGATGATATACCTCCAACTTTATGATAGTGTGCTTCCAAATGTT 963
QY 901 GTCCGTATTTTAAAGACATATCTTCCGATGCTTGAAGAGAGATATGAGATT 960
DB 964 GTCCGTATTTTAAAGACATATCTTCCGATGCTTGAAGAGAGATATGAGATT 1023
QY 961 AGACATGTTGGGAGACGCTCACCAGATTAACAAATTAAGTGTGCTTCCAGTTG 1017
DB 1024 AGACATGTTGGGAGACGCTCACCAGATTAACAAATTAAGTGTGCTTCCAGTTG 1080

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RESULT 3

AA07067 standard; cDNA; 1193 BP.

AD07067;

06-AUG-2001 (first entry)

Human six transmembrane epithelial antigen of prostate-1 clone 10 cDNA.

Human; cytosolic; antiproliferative; vaccine; gene therapy;

six transmembrane epithelial antigen of the prostate-1; STRAP-1;

chromosome 7p22.3; cancer; prostate; colon; bladder; lung; ovarian;

pancreatic; ss.

Homo sapiens.

Key

CDS

Location/Qualifiers

64..1191

/*tag= a

/product= "Human six transmembrane epithelial antigen of

the prostate (STRAP)-1"

/note= "CDS does not include stop codon"

/transl_except= (pos:1078..1086, aa:Leu-Aasn)

/note= "inframe stop codon alters the reading frame"

/partial

MO200140276-A2.

07-JUN-2001.

06-DEC-2000; 2000MO-US033040.

06-DEC-1999; 99US-00455486.

(UROG-) UROGENESYS INC.

Afar DEH, Hubert RS, Raitano AB, Saffran DC, Mitchell SC;

Faris M, Jakobovits A;

WPI: 2001-367804/38.

P-PSDB; AAE02780.

New STRAP (six transmembrane epithelial antigen of the prostate)

proteins, expressed in human cancers, useful for detecting and treating

cancer.

Example 2; Fig 1A-1B; 187bp; English.

The present sequence is human six transmembrane epithelial antigen of the

prostate (STRAP)-1 clone 10 cDNA. STRAP-1 gene is located on chromosome

7p22.3 and is used in gene therapy. Inhibiting the development or

progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and

pancreatic) expressing STRAP or inhibiting growth or killing cells

expressing STRAP in a patient, comprises administering a vaccine

composition to the patient. Treating a patient with a cancer that

Db 126 AATTAAAGAGAGCGATTATTTGACATAGAGACGAGAGACACACATGCTAAAGAA 185
 QY CTTGTCCTTTGACATTTGACCAAAAGCCCATGATGATTTGACTGCGCTTGAA 180
 Db 186 CTTGTCCTTTGACATTTGACCAAAAGCCCATGATGATTTGACTGCGCTTGAA 245
 QY 181 CTTGACGACACAGAACTCTTTCACAGTGGCACTTGGCAATTAATAGTCTATT 240
 Db 246 CTTGACGACACAGAACTCTTTCACAGTGGCACTTGGCAATTAATAGTCTATT 305
 QY 241 ATAGCATCTGACTTTTCTTTACACTCTTGTGAGGAAAGTAACTACCTTTAGCACT 300
 Db 306 ATAGCATCTGACTTTTCTTTACACTCTTGTGAGGAAAGTAACTACCTTTAGCACT 365
 QY 301 TCCCATCAACAAATTTTAAATTCGAATCTGTCATCAACAAAGCTTGGCAATG 360
 Db 366 TCCCATCAACAAATTTTAAATTCGAATCTGTCATCAACAAAGCTTGGCAATG 425
 QY 361 GTTTCATCACTCTCTTGGCACTTGTATCTGCAAGTGTGATAGCAGCAATTTGCCAA 420
 Db 426 GTTTCATCACTCTCTTGGCACTTGTATCTGCAAGTGTGATAGCAGCAATTTGCCAA 485
 QY 421 CTTTCATTAATGGAACCAAGTAAAGAGTTTCCACATTTGTTGATTAAGTAACTAACA 480
 Db 486 CTTTCATTAATGGAACCAAGTAAAGAGTTTCCACATTTGTTGATTAAGTAACTAACA 545
 QY 481 AGAAGACAGTTGGGGCTCTGACATTTCTTTTGTGCTGATGATGATGATTAATGAGCTG 540
 Db 546 AGAAGACAGTTGGGGCTCTGACATTTCTTTTGTGCTGATGATGATGATTAATGAGCTG 605
 QY 541 TCTTACCAATGAGGCGATCTCAAGTAAAGTGTAACTGGGCACTATCAACAGCTG 600
 Db 606 TCTTACCAATGAGGCGATCTCAAGTAAAGTGTAACTGGGCACTATCAACAGCTG 665
 QY 601 CAACAAATTAAGAGATGCTGGATTGAGCATGATGTTTGAAGATGAGATTTATGTC 660
 Db 666 CAACAAATTAAGAGATGCTGGATTGAGCATGATGTTTGAAGATGAGATTTATGTC 725
 QY 661 TCTCTGGGAATGTTGGGATTTGGGAATGAGTGGCTGTTGGCTGATCATTTATTCATCT 720
 Db 726 TCTCTGGGAATGTTGGGATTTGGGAATGAGTGGCTGTTGGCTGATCATTTATTCATCT 785
 QY 721 GTGAGTGAATCTTTGACATGAGAGAAATTCACATATTTGAGAGCAAGCTAGGAATTTGTT 780
 Db 786 GTGAGTGAATCTTTGACATGAGAGAAATTCACATATTTGAGAGCAAGCTAGGAATTTGTT 845
 QY 781 TCCCTTTCTACTGGGCAATATACAGCATTTGTTTCTGGAATTAAGTATGATATATA 840
 Db 846 TCCCTTTCTACTGGGCAATATACAGCATTTGTTTCTGGAATTAAGTATGATATATA 905
 QY 841 AAACAAATTTGATGATATACCTCCAACTTTATGATAGCTGTTTCTTCCAAATTTGTT 900
 Db 906 AAACAAATTTGATGATATACCTCCAACTTTATGATAGCTGTTTCTTCCAAATTTGTT 965
 QY 901 GTCTGATATTTAAAGCACTATCTCTGCGCATGCTTGAAGAAAGATTAAGTATGAGATT 960
 Db 966 GTCTGATATTTAAAGCACTATCTCTGCGCATGCTTGAAGAAAGATTAAGTATGAGATT 1025
 QY 961 AGACATGTTGGGAGAGCTCAACAAATTAACAAATGAGATATGTTCCCAAGTTG 1017
 Db 1026 AGACATGTTGGGAGAGAGCTCAACAAATTAACAAATGAGATATGTTCCCAAGTTG 1082

RESULT 5
 ADY92698
 ID ADY92698 standard; cDNA; 1193 BP.
 AC ADY92698;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Human STEAP-1 (8p1B4) clone 10 cDNA, SEQ ID NO: 1.

XX Vaccine; antibody therapy; immune stimulation; gene amplification;
 KM prostate tumor; cytostatic; andrology; genitourinary disease; neoplasm;
 KM cancer; six transmembrane epithelial antigen of prostate 1; STEAP-1;
 KW chromosome 7; gene; B6.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 64..1191
 FT /tag= b
 FT /product= "Human STEAP-1 protein #2"
 FT /transl_except= (pos:1078..1086, aa:Leu-Asn)
 FT /partial
 FT /note= "No stop codon"
 FT CDS 64..1083
 FT /tag= a
 FT /product= "Human STEAP-1 protein #1"
 XX
 PN US2005063975-A1.
 XX
 PD 24-MAR-2005.
 XX
 PF 05-JAN-2004; 2004US-00752421.
 XX
 PR 01-JUN-1999; 99US-00323873.
 PR 06-DEC-1999; 99US-00455486.
 XX
 PA (AFAP/) AFAP D E H.
 PA (HUBE/) HUBERT R S.
 PA (RAIT/) RAITANO A B.
 PA (SAFE/) SAFRAN D.
 PA (MITC/) MITCHELL S C.
 XX
 PI Afar DEH, Hubert RS, Raitano AB, Safran D, Mitchell SC;
 DR MPI; 2005-252610/26.
 DR P-PSDB; ADY92699, ADY92744.
 XX
 PT Novel isolated polynucleotide that encodes six transmembrane epithelial
 PT antigen of prostate polypeptide, useful for diagnosing or treating
 PT prostate cancer.
 XX
 PS Example 1; SEQ ID NO 1; 80bp; English.
 XX
 CC The invention relates to cell surface serpentine transmembrane antigens
 CC predominantly expressed in the prostate termed as six transmembrane
 CC epithelial antigen of prostate (STEAP-2) and their corresponding nucleic
 CC acid sequences. STEAP-2 DNA is useful for diagnosing or treating prostate
 CC cancer. It can be used as a primer or probe for the amplification and/or
 CC detection of STEAP genes and as a tool for modulating or inhibiting the
 CC expression of the STEAP genes. STEAP-2 DNA is also useful in cancer
 CC vaccines for the generation of therapeutic or prophylactic immunity
 CC against prostate cancer. STEAP antibodies are useful in antibody therapy.
 CC The present sequence is the human STEAP-1 cDNA. Human STEAP-1 gene maps
 CC within chromosome 7p22 (7p2.3).
 XX
 SQ Sequence 1193 BP; 382 A; 219 C; 233 G; 359 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1017; DB 14; Length 1193;
 Best Local Similarity 100.0%; Pred. No. 2,6e-276;
 Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX	WO200151633-A2.
PN	
PD	19-JUL-2001.
PF	16-JAN-2001; 2001WO-US001574.
PX	
PR	14-JAN-2000; 2000US-00483672.
PA	(CORI-) CORIXA CORP.
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,
PI	Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAW;
PI	Wang A, Meagher MJ;
XX	
XX	WPI, 2001-425873/45.
DR	
XX	New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT	monitoring and treating prostate cancer in a patient and for use in
PT	vaccines.
XX	
PS	Claim 1; Page 510; 543pp; English.
XX	
CC	The present invention describes polynucleotide sequences (I) which encode
CC	prostate-specific proteins (II). (I) and (II) have cytosolic activity,
CC	and can be used in vaccine production and gene therapy. (I), (II),
CC	antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC	prepared using (I) or (II) are used treat cancer in a patient. (I) and
CC	the antibodies are also used in the detection of cancer in a patient. (I)
CC	cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC	and (II) can be used in vaccines. The antibodies or (I) can be used for
CC	monitoring the progression of cancer in a patient. (I) and (II) can also
CC	be used to improve diagnostic and therapeutic methods for prostate
CC	cancer. They can indicate the level of metastasis as well as the prostate
CC	cancer. volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent
CC	polynucleotide and amino acid sequences used in the exemplification of
CC	the present invention
SQ	
	Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
	Query Match 100.0%; Score 1017; DB 4; Length 1195;
	Best Local Similarity 100.0%; Pred. No. 2.6e-276;
	Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY	1 ATGGAAGACGAAAAAGACATCAAAACCAGAAGAACTTTGGAAAATAAGCTGTAGAGA 60
DB	66 ATGGAAGACGAAAAAGACATCAAAACCAGAAGAACTTTGGAAAATAAGCTGTAGAGA 125
DB	126 AATTTAGAAGAAAGACGATTATTTCGATTAAGACAACGCGAGAGAACGACATGTATAAAGA 185
QY	61 AATTTAGAAGAAAGACGATTATTTCGATTAAGACAACGCGAGAGAACGACATGTATAAAGA 120
QY	121 CCTGTGCTTTTGCAATTTGGCACCMAACGCCCATGTGATGAATTTGACTGCCCTTACAGA 180
DB	186 CCGTGTCTTTTGCAATTTGGCACCMAACGCCCATGTGATGAATTTGACTGCCCTTACAGA 245
QY	181 CTTCAGACACACAGGAATCTTTTCCACAGTGGCACTTGCACAAATTAATAGCTGTATT 240
DB	246 CTTCAGACACACAGGAATCTTTTCCACAGTGGCACTTGCACAAATTAATAGCTGTATT 305
QY	241 ATNAGATCTCTGACTTTCTTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAGCACT 300
DB	306 ATNAGATCTCTGACTTTCTTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAGCACT 365
QY	301 TCCCATCAACAATTTTTATATAAATTCCAATCTGTGTCATCAACAAAGCTTTGCCAATG 360
DB	366 TCCCATCAACAATTTTTATATAAATTCCAATCTGTGTCATCAACAAAGCTTTGCCAATG 425
QY	361 GTTTCATCACTCTCTTGGCATTTGTTTACCTGCGCAGGTGTGATAGCACAAATTGTCGA 420
DB	426 GTTTCATCACTCTCTTGGCATTTGTTTACCTGCGCAGGTGTGATAGCACAAATTGTCGA 485
QY	421 CTTTCATTAATGGAACCAAGTATAGAAGTTTCCACATTTGTTGGATTAGTGATGTTTAACA 480

D	b		486	CTTCATATTGGAACCAAGTATTAAGAAGTTCCACATGTGGTAGTAAGTGAAATGTTAACA	545
O	y		481	AGAAAAGCAGTTTGGGCTTCTCGAGTTCTTTTTTGCCTGTACTGCAATGCAATTAATAGTCTG	540
D	b		546	AGAAAGCAGTTTGGGCTTCTCGAGTTCTTTTTTGCCTGTAAGTCAAGCAATTAATAGTCTG	605
O	y		541	TCTTAACCAATGAGGCGATGCCATACAGATAACAAGTTGCTAAACTGGGCAATCAACAGGTC	600
D	b		606	TCTTAACCAATGAGGCGATCCTACAGATACAAAGTTGCTAAACTGGGCAATCAACAGGTC	665
O	y		601	CACAAAAATAAAGAAGATCCCTGATGTAAGCATGATGTTTGGAGATGAGATTTATGTG	660
D	b		666	CACAAAAATAAAGAAGATCCCTGATGTAAGCATGATGTTTGGAGATGAGATTTATGTG	725
O	y		661	TCTCTGGGAATTTGGGAGTTGGCAATTACGCGCTGTTGGGCTGGTAGCAATTAATTCATCT	720
D	b		726	TCTCTGGGAATTTGGGAGTTGGCAATTACGCGCTGTTGGGCTGGTAGCAATTAATTCATCT	785
O	y		721	GTVGATGACTCTTTGACATGAGAGAAATTCCTACTATATTTCAGAGCAAGCTAGGAATGTT	780
D	b		786	GTVGATGACTCTTTGACATGAGAGAAATTCCTACTATATTTCAGAGCAAGCTAGGAATGTT	845
O	y		781	TCCCTTTCTACTGGGCACAATACAGCANTGATTTTGGCTGGAAATAGTGATAGATATA	840
D	b		846	TCCCCTTTCTACTGGGCACAATACAGCANTGATTTTGGCTGGAAATAGTGATAGATATA	905
O	y		841	AACAAATTTGATGGTATACACCTTCAACTTTATGATAGCTGTTTCCCTCCAATGTT	900
D	b		906	AACAAATTTGATGGTATACACCTTCAACTTTATGATAGCTGTTTCCCTCCAATGTT	965
O	y		901	GTCTGTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAAGAGAAATCTGAAGATT	960
D	b		966	GTCTGTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAAGAGAAATCTGAAGATT	1025
O	y		961	AGACATGGTTGGGAAGAGCTCACCAAAATTTAACAAACTGAGATATGTTCCCAAGTTG	1017
D	b		1026	AGACATGGTTGGGAAGAGCTCACCAAAATTTAACAAACTGAGATATGTTCCCAAGTTG	1082
RESULT 7					
ID			AAS64160	AAS64160 standard; cDNA, 1195 BP.	
XX AC			AAS64160;		
XX DT			29-JAN-2002 (first entry)		
XX DE			Human prostate cDNA sequence #590.		
XX KW			Human; prostate cancer; ss; cytolethic; immunostimulant; tumour.		
XX OS			Homo sapiens.		
XX NN			WO200173032-A2.		
XX PD			04-OCT-2001.		
XX PF			27-MAR-2001; 2001MO-US0009919.		
XX PR			27-MAR-2000; 2000US--00536857.		
XX PR			09-MAY-2000; 2000US--00568100.		
XX PR			12-MAY-2000; 2000US--00570737.		
XX PR			13-JUN-2000; 2000US--00583793.		
XX PR			27-JUN-2000; 2000US--00605783.		
XX PR			09-AUG-2000; 2000US--00636215.		
XX PR			29-AUG-2000; 2000US--00651236.		
XX PR			06-SEP-2000; 2000US--00657279.		
XX PR			02-OCT-2000; 2000US--00679426.		
XX PR			10-OCT-2000; 2000US--00685166.		
XX PR			09-NOV-2000; 2000US--00709729.		
XX PA			(CORI-) CORIXA CORP.		

Pt	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
Pt	Fanger GR, Retzer MW, Stolk JA, Day CH, Vedvick TS, Carter D;
Pt	Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;
XX	WPJ, 2001-639232/73.
DR	P-PSDB; MAU69927.
XX	
Pt	New human prostate-specific polypeptides and polynucleotides useful for
Pt	the diagnosis and treatment of cancer, especially prostate cancer.
XX	
Ps	Claim 1, Page 548; 579pp; English.
XX	
Cc	The invention relates to isolated prostate-specific polynucleotides,
Cc	polypeptides, fusion proteins of the polypeptides, antibodies raised
Cc	against the polypeptides (or antigenic epitopes derived from them) and
Cc	antigen-presenting cells expressing the polypeptides. The antibodies are
Cc	useful for detecting the presence of cancer, especially prostate cancer.
Cc	The polypeptides, polynucleotides and the antigen-presenting cells are
Cc	useful for stimulating and/or expanding T cells specific for a tumour
Cc	protein, and for inhibiting the development of cancer especially prostate
Cc	cancer. Compositions comprising the polynucleotide and/or polypeptide are
Cc	useful for stimulating an immune response, and for treating cancer. The
Cc	oligonucleotide is useful for detecting cancer. The present sequence is a
Cc	prostate specific polynucleotide of the invention
SQ	
	Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
	Query Match: 100.0%; Score 1017; DB 4; Length 1195;
	Best Local Similarity: 100.0%; Pred. No. 2, 6e-276; Mismatches 0; Indels 0; Gaps 0
	Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	1 ATGMAAGCAGAAAAAATCATCAAAACCAAGAAGACTTTGGAAAATGAAGCTTAGAGA 60
Dd	66 ATGMAAGCAGAAAAAATCATCAAAACCAAGAAGACTTTGGAAAATGAAGCTTAGAGA 125
Oy	61 AATTTAAGAAGAACGATTATTTCGATTAAGACAACGGAGAGACCAGATGCTAAAGA 120
Dd	126 AATTTAAGAAGAACGATTATTTCGATTAAGACAACGGAGAGACCAGATGCTAAAGA 185
Oy	121 CCTGTGCCTTGGACATTTTGACCAAACAGCCCATCTGATGAATTTGACCTTCAGNA 180
Dd	186 CCTGTGCCTTGGACATTTTGACCAAACAGCCCATCTGATGAATTTGACCTTCAGNA 245
Oy	181 CTTCAGCACACAGAACTCTTTCACAGTGGCACTTGGCCAATTAATAATGCTCTATT 240
Dd	246 CTTCAGCACACAGAACTCTTTCACAGTGGCACTTGGCCAATTAATAATGCTCTATT 305
Oy	241 ATTACATCTCGACTTTTCTTTTACACTCTTCAGGGGAAGTAATCACCCCTTAGCACT 300
Dd	306 ATTACATCTCGACTTTTCTTTTACACTCTTCAGGGGAAGTAATCACCCCTTAGCACT 365
Oy	301 TCCCATGAACAATATTTTTATMAAATTCGAATCCGTGATCAACAAAGCTTGCCAATG 360
Dd	366 TCCCATGAACAATATTTTTATMAAATTCGAATCCGTGATCAACAAAGCTTGCCAATG 425
Oy	361 GTTTTCATCACTCTCTTGGCATTTGGTTTACCTGCCAGGTGTGATAGAGCAATGTCCAA 420
Dd	426 GTTTTCATCACTCTCTTGGCATTTGGTTTACCTGCCAGGTGTGATAGAGCAATGTCCAA 485
Oy	421 CTTGATATATGAACCAAGATATMAAGTTTCCATTGGTTGATTAAGTATTTTAAACA 480
Dd	486 CTTGATATATGAACCAAGATATMAAGTTTCCATTGGTTGATTAAGTATTTTAAACA 545
Oy	481 AGAAAGCAGTTGGGCTTCTCAATTTCTTTTGGCTGATCTGATGCAATTTATAGTCTG 540
Dd	546 AGAAAGCAGTTGGGCTTCTCAATTTCTTTTGGCTGATCTGATGCAATTTATAGTCTG 605
Oy	541 TCTTAACCAATGAAGGCATCTTACAGATATCAAGTTGTAAACTGGGCTATCAACAGTTC 600
Dd	606 TCTTAACCAATGAAGGCATCTTACAGATATCAAGTTGTAAACTGGGCTATCAACAGTTC 665
Oy	601 CAACAAATTAAGAAGATGCTCGATGTGAGCATGATGTTTGGAGATGGAAGATTTATGTG 660

```

Db      666 CAAACAAATTAAGAGATGCTGATGATGAGCATGATGTTGGAGATGAGATTTATG 725
Qy      661 TCTCTGGGAATTTGGGATTTGGCAATATCTGCTGTGGCTGTGAATCTATTCACATCT 720
Db      726 TCTCTGGGAATTTGGGATTTGGCAATATCTGCTGTGGCTGTGAATCTATTCACATCT 785
Qy      721 GAGAGCATCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATTTG 780
Db      786 GTGAGGACCTTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATTTG 845
Qy      781 TCCCTTCTACTGGGCAATATACGAGATGATTTTGGCTGTGAATATGATGATATATA 840
Db      846 TCCCTTCTACTGGGCAATATACGAGATGATTTTGGCTGTGAATATGATGATATATA 905
Qy      841 AAACAAATTTGTATGATATACCTCCACCTTTTATGATAGCTGTTTCCCTCAATTTG 900
Db      906 AAACAAATTTGTATGATATACCTCCACCTTTTATGATAGCTGTTTCCCTCAATTTG 965
Qy      901 GTCTGTATATTTTAAAGCATATCTATCTGCTGCTGTGAGAGAAAGATCTGAAGATT 960
Db      966 GTCTGTATATTTTAAAGCATATCTATCTGCTGCTGTGAGAGAAAGATCTGAAGATT 1025
Qy      961 AGACATGTTGGGAGACGTCACCAAAATTTACAAAGCTGATGTTCCCGAGTTG 1017
Db      1026 AGACATGTTGGGAGACGTCACCAAAATTTACAAAGCTGATGTTCCCGAGTTG 1082

RESULT 8
ACAS9968
ID ACAS9968 standard; cDNA; 1195 BP.
XX
AC ACAS9968;
XX
XX
XX 10-JUN-2003 (first entry)
XX
XX
XX Prostate cancer therapy associated cDNA #655.
DE
XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
XX immunogen; cancer; prostate specific antigen; PSA;
XX prostatic acid phosphatase; PAP; prostate specific membrane antigen;
XX PSMa; gene; ss.
XX
XX Homo sapiens.
XX
XX US2002192763-A1.
XX
XX 19-DEC-2002.
XX
XX 29-JUN-2001; 2001US-00895793.
XX
XX 04-OCT-1999; 99US-0157455P.
XX 04-OCT-2000; 2000US-00679272.
XX 28-MAR-2001; 2001US-00822827.
XX
XX (XUJ/) XU J.
XX (DILL/) DILLON D C.
XX (MITC/) MITCHAM J L.
XX (HARL/) HARLOCKER S L.
XX (JIANG/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
XX (STOL/) STOLK J A.
XX (DAYC/) DAY C H.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (LISK/) LI S X.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y A W.
XX (HEPL/) HEPLER W T.
XX (HEND/) HENDERSON R A.
XX (HURA/) HURAL J.

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PA (MCNE/) MCNEILL P D.
PA (HONG/) HONGTUN R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SH, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI McNeill PD, Houghton RL, Y De Bassolsey, Foy TM;
XX
XX WPI; 2001-245062/25.
DR P-PSDB; ABU71821.
XX
XX Prostate specific protein and its encoding polynucleotide, useful for the
PT treatment and diagnosis of prostate cancer.
XX
XX Example 5; SEQ ID NO 878; 85bp; English.
XX
XX The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 3 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This sequence represents a prostate cancer
CC therapy associated cDNA. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the US patent office at
CC segdata.uspto.gov/sequence.html?docID=US20020192763
XX
XX SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 1017; DB 5; Length 1195;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-276;
XX Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 ATGGAAGCAGAAAGACATCAACCAAGAGAACTTTGGAAATGAAAGCTTAGAGA 60
Db 66 ATGGAAGCAGAAAGACATCAACCAAGAGAACTTTGGAAATGAAAGCTTAGAGA 125
Qy 61 AATTTAGAGAGAGAGATTTATTTGATAGAGACAGGAGAGACAGCATGCTTAAAAA 120
Db 126 AATTTAGAGAGAGAGATTTATTTGATAGAGACAGGAGAGACAGCATGCTTAAAAA 185
Qy 121 CCTGTCTTTTGCAATTTGACCAACAGCCCATGCTGATGATTTGACTGCCCTTCA 180
Db 186 CCTGTCTTTTGCAATTTGACCAACAGCCCATGCTGATGATTTGACTGCCCTTCA 245
Qy 181 CTTGACGACACAGAGAACTTTTCCACAGTGGCACTTGCCTTCAATTTAACTCTATT 240
Db 246 CTTGACGACACAGAGAACTTTTCCACAGTGGCACTTGCCTTCAATTTAACTCTATT 305
Qy 241 ATGACATCTGACTTTTCTTACACTCTTTCAGAGGAATTAATCACCCCTTAGCACT 300
Db 306 ATGACATCTGACTTTTCTTACACTCTTTCAGAGGAATTAATCACCCCTTAGCACT 365
Qy 301 TCCCATCAACAATATTTTATATAAATTCATCTGCTGATCATCAACAAGCTTTGCAATG 360
Db 366 TCCCATCAACAATATTTTATATAAATTCATCTGCTGATCATCAACAAGCTTTGCAATG 425
Qy 361 GTTTCATCATCTCTCTTGGCATTTGTTTACCTGCGCAGAGTGTATAGCAGCAATTTGCCAA 420
Db 426 GTTTCATCATCTCTCTTGGCATTTGTTTACCTGCGCAGAGTGTATAGCAGCAATTTGCCAA 485
Qy 421 CTTCAATATGAGAACCAAGTATAGAGTTTCCATGTTGGTATAGTATGATTAACA 480
Db 486 CTTCAATATGAGAACCAAGTATAGAGTTTCCATGTTGGTATAGTATGATTAACA 545
Qy 481 AGAAGCAGTTTGGCTTCTCAGTTTCTTTTGTGTAATGATGCAATTTAATAGCTTG 540
Db 546 AGAAGCAGTTTGGCTTCTCAGTTTCTTTTGTGTAATGATGCAATTTAATAGCTTG 605

```

QY 541 TCTTACCAATGAGCGCATCTTACAGATACAAAGTTGGCTAAACTGGGATATCAACAGGTC 600
DB 606 TCTTACCAATGAGCGCATCTTACAGATACAAAGTTGGCTAAACTGGGATATCAACAGGTC 665
QY 601 CAACAAATTAAGAAGATGCTTGGATGAGCATGATGTTGGAGATGAGATTTATGTG 660
DB 666 CAACAAATTAAGAAGATGCTTGGATGAGCATGATGTTGGAGATGAGATTTATGTG 725
QY 661 TCTCTGGAAATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 720
DB 726 TCTCTGGAAATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 785
QY 721 GTGAGTACTCTTTCAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 780
DB 786 GTGAGTACTCTTTCAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 845
QY 781 TCCCTTCTACTGGGACAAATACAGCATGATGATTTTGGCTGGAAATTAAGTGAATGATATA 840
DB 846 TCCCTTCTACTGGGACAAATACAGCATGATGATTTTGGCTGGAAATTAAGTGAATGATATA 905
QY 841 AAACAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 906 AAACAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 965
QY 901 GTCTGATATTTTAAAGCATATCTATTCCTGCGCATGCTTGAAGAGAGATGATGAGATT 960
DB 966 GTCTGATATTTTAAAGCATATCTATTCCTGCGCATGCTTGAAGAGAGATGATGAGATT 1025
QY 961 AGACATGCTGGGAG 1017
DB 1026 AGACATGCTGGGAG 1082

RESULT 9

ABL95531 standard; cDNA; 1195 BP.

ABL95531;

19-JUL-2002 (first entry)

Human P789P cDNA sequence SEQ ID NO 878.

Human: cancer; prostate cancer; vaccine; cytostatic; immunostimulant;

gene therapy; gene; ss.

Homo sapiens.

US2002022248-A1.

21-FEB-2002.

12-JAN-2001; 2001US-00759143.

25-FEB-1997; 97US-00806099.

10-FEB-1998; 97US-00904804.

25-FEB-1998; 98US-00030607.

14-JUL-1998; 98US-00115453.

23-SEP-1998; 98US-00159812.

15-JAN-1999; 99US-00232149.

09-APR-1999; 99US-00288946.

13-JUL-1999; 99US-00352616.

12-NOV-1999; 99US-00433913.

14-JAN-2000; 2000US-00483672.

27-MAR-2000; 2000US-00536857.

09-MAY-2000; 2000US-00568100.

12-MAY-2000; 2000US-00570737.

13-JUN-2000; 2000US-00593793.

27-JUN-2000; 2000US-00605783.

10-AUG-2000; 2000US-00636215.

PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.

(XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.

XU J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA; WPI; 2002-255649/30.

New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer.

Claim 1; SEQ ID NO 878; 87pp; English.

The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention

Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1017; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2,6e-276;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAAG 60
DB 66 ATGGAAG 125
QY 61 AATTGAG 120
DB 126 AATTGAG 185
QY 121 CCTGTGCTTTTGATTTGACCAACAGCCATGCTGATGAATTTGACTGCCCCCTTGAGAA 180
DB 186 CCGTGCTTTTGATTTGACCAACAGCCATGCTGATGAATTTGACTGCCCCCTTGAGAA 245
QY 181 CTTGAG 240
DB 246 CTTGAG 305
QY 241 ATGAGATCTGTGCTTTGCTTACACTCTTGGAGGAGATTAATCACCCCTTGAAGACT 300
DB 306 ATGAGATCTGTGCTTTGCTTACACTCTTGGAGGAGATTAATCACCCCTTGAAGACT 365
QY 301 TCCATCAACAATATTTTAAATTCATCTGCTGATCAACAAGCTTTGCAATG 360
DB 366 TCCATCAACAATATTTTAAATTCATCTGCTGATCAACAAGCTTTGCAATG 425
QY 361 GTTTCATCACTCTGTTGGATTTGTTACCTGCGAGGAGTGTATGACAGCAATTTGCCAA 420
DB 426 GTTTCATCACTCTGTTGGATTTGTTACCTGCGAGGAGTGTATGACAGCAATTTGCCAA 485

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QY 421 CTTTCAATTAATGGAACCAAGTATTAAGATTTCACATTTGGTGGATTAAGTATGTTAACA 480
DB 486 CTTTCAATTAATGGAACCAAGTATTAAGATTTCACATTTGGTGGATTAAGTATGTTAACA 545
QY 481 AGAAAGCAAGTTGGGCTTCTGATTTCTTTTGGCTGTACTGCAATTTATATAGTCG 540
DB 546 AGAAAGCAAGTTGGGCTTCTGATTTCTTTTGGCTGTACTGCAATTTATATAGTCG 605
QY 541 TCTTACCCCAATGAGGCGATCCTAAGATCAAGATTGCTAACTGGGCAATCAACAGTGC 600
DB 606 TCTTACCCCAATGAGGCGATCCTAAGATCAAGATTGCTAACTGGGCAATCAACAGTGC 665
QY 601 CAACAAATTAAGAAAGATGCTTGATTTGAGCATGATGTTTGAAGATGGAATTTATGTCG 660
DB 666 CAACAAATTAAGAAAGATGCTTGATTTGAGCATGATGTTTGAAGATGGAATTTATGTCG 725
QY 661 TCTTGGGGAATTTGGGATTTGGCAATATCTGGCTCTGTTGGCTGTGACATCTTATTCATCT 720
DB 726 TCTTGGGGAATTTGGGATTTGGCAATATCTGGCTCTGTTGGCTGTGACATCTTATTCATCT 785
QY 721 GTGAGTGAATCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATTTGT 780
DB 786 GTGAGTGAATCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATTTGT 845
QY 781 TCCCTTCTACTGAGGCACAATTAACCGCATTTGTTTGCCTGGAATTAAGTATAGATATA 840
DB 846 TCCCTTCTACTGAGGCACAATTAACCGCATTTGTTTGCCTGGAATTAAGTATAGATATA 905
QY 841 AAACAATTTGTATGTATGATACCTCCAACTTTATATATAGCTGTTTCTTCCCAATTTGT 900
DB 906 AAACAATTTGTATGTATGATACCTCCAACTTTATATATAGCTGTTTCTTCCCAATTTGT 965
QY 901 GTTCGATATTTTAAAGCATATCTATCTGCGCATGCTTGAAGAAAGATCTGAAGATT 960
DB 966 GTTCGATATTTTAAAGCATATCTATCTGCGCATGCTTGAAGAAAGATCTGAAGATT 1025
QY 961 AGACATGTGTTGGGAAGACGTCAACCAAAATTAACAAAAGTGAATATGTTCCAGTTG 1017
DB 1026 AGACATGTGTTGGGAAGACGTCAACCAAAATTAACAAAAGTGAATATGTTCCAGTTG 1082

RESULT 10
ABK92128
ID ABK92128 standard; DNA; 1195 BP.
XX
AC ABK92128;
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated DNA sequence #14.
XX
KM Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
XX gene therapy; gene; db.
XX
OS Mammalia.
XX
PN WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032045.
XX
PR 13-OCT-2000; 2000US-00687576.
XX
PR 08-DEC-2000; 2000US-00733288.
XX
PR 08-DEC-2000; 2000US-00733742.
XX
PR 24-JAN-2001; 2001US-0263957P.
XX
PR 16-MAR-2001; 2001US-0276791P.
XX
PR 16-MAR-2001; 2001US-0276888P.
XX
PR 06-APR-2001; 2001US-0281922P.
XX
PR 24-APR-2001; 2001US-0286214P.
XX
PR 30-APR-2001; 2001US-00847046.
XX
PR 04-MAY-2001; 2001US-0288589P.
```

```
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
DR MPI: 2002-471335/50.
XX
DR P-PSDB; AB661813.
XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
XX
PS Claim 22; Page 311-312; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridize to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 1017; DB 6; Length 1195;
Query Local Similarity 100.0%; Pred. No. 2.6e-276;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAAGCAGAAAAGACATCAACAAACCAAGAACTTTGGAAATGAAGCTTAGAGA 60
DB 66 ATGGAAGCAGAAAAGACATCAACAAACCAAGAACTTTGGAAATGAAGCTTAGAGA 125
QY 61 AATTTAGAAGAAAGATATTTTGCATTAAGACAAGGGAGAGACAGATGCTAAAAAGA 120
DB 126 AATTTAGAAGAAAGATATTTTGCATTAAGACAAGGGAGAGACAGATGCTAAAAAGA 185
QY 121 CCTGTGCTTTTGCATTTGCAACCAACAGCCCATGCTGAATTTGACTGCGCTTCAGAA 180
DB 186 CCTGTGCTTTTGCATTTGCAACCAACAGCCCATGCTGAATTTGACTGCGCTTCAGAA 245
QY 181 CTTCAGCACACACAGAACTTTTCCACAGTGGCACTTGCATTTAAATATAGCTGTATT 240
DB 246 CTTCAGCACACACAGAACTTTTCCACAGTGGCACTTGCATTTAAATATAGCTGTATT 305
QY 241 ATAGCATCTGTGACCTTTCTTACACTCTTCTGAGGGAAGTAATCACCTTTAGCAACT 300
DB 306 ATAGCATCTGTGACCTTTCTTACACTCTTCTGAGGGAAGTAATCACCTTTAGCAACT 365
QY 301 TCCCATCAACATATTTTAAATTCATCTGTGCATCAACAAGTCTTGGCAATG 360
DB 366 TCCCATCAACATATTTTAAATTCATCTGTGCATCAACAAGTCTTGGCAATG 425
QY 361 GTTTCATCACTCTCTTGGCATTTGTTTACTGCAAGTGTATGACGAATTTGCCAA 420
DB 426 GTTTCATCACTCTCTTGGCATTTGTTTACTGCAAGTGTATGACGAATTTGCCAA 485
QY 421 CTTTCAATTAATGGAACCAAGTATTAAGATTTCACATTTGGTGGATTAAGTATGTTAACA 480
DB 486 CTTTCAATTAATGGAACCAAGTATTAAGATTTCACATTTGGTGGATTAAGTATGTTAACA 545
QY 481 AGAAAGCAAGTTGGGCTTCTGATTTCTTTTGGCTGTACTGCAATTTATATAGTCG 540
DB 546 AGAAAGCAAGTTGGGCTTCTGATTTCTTTTGGCTGTACTGCAATTTATATAGTCG 605
```

QY	541	TCCTAACCAATGAGCGGATCCCTACAGATACAGGTTGCTAACTGGGCATATCAAGATC	600
Db	606	TCTTACCATATAGGAGGATCTTACAGATACAAAGTTGCTAACTGGGCATATCAAGGTC	665
QY	601	CAACAAATTAAGGAAGATGCCGTGATTGAGCATGTATGTTGGAGATGAGATTTATGTG	660
Db	666	CAACAAATTAAGGAAGATGCCGTGATTGAGCATGTATGTTGGAGATGAGATTTATGTG	725
QY	661	TCTCTGGGAATGTGGGATTTGGCAATACGTGGCTCTGTTGGCTGTGACATCTATTCACCT	720
Db	726	TCTCTGGGAATGTGGGATTTGGCAATACGTGGCTCTGTTGGCTGTGACATCTATTCACCT	785
QY	721	GTGATGCACTCTTTGACATGAGAGAATTTCACTATATTCAGAGCAAGCTAGAAATGTT	780
Db	786	GTGATGCACTCTTTGACATGAGAGAATTTCACTATATTCAGAGCAAGCTAGAAATGTT	845
QY	781	TCCCTCTTACTGGGCAACAATACAGCGATTTGTTGCCGTGAAATAGTGATAGATATA	840
Db	846	TCCCTCTTACTGGGCAACAATACAGCGATTTGTTGCCGTGAAATAGTGATAGATATA	905
QY	841	AAACAATTTGATGTGATACATCTCCACTTTATGATAGCGTTTCCCTCCATTTGTT	900
Db	906	AAACAATTTGATGTGATACATCTCCACTTTATGATAGCGTTTCCCTCCATTTGTT	965
QY	901	GTCTGATATTTAAAGCATACTATTTCTGCCATGCTTGAGGAGAAAGATACGAAAGTT	960
Db	966	GTCTGATATTTAAAGCATACTATTTCTGCCATGCTTGAGGAGAAAGATACGAAAGTT	1025
QY	961	AGACATGTTGGGAAGAGCTGACCAAAATTAACAAACTGAGATATGTTCCCAAGTTG	1017
Db	1026	AGACATGTTGGGAAGAGCTGACCAAAATTAACAAACTGAGATATGTTCCCAAGTTG	1082

PT	RESULT 11
XX	ACC95695
ID	ACC95695 standard; cDNA, 1195 BP.
XX	
AC	ACC95695;
XX	
DT	28-AUG-2003 (first entry)
XX	
DE	Prostate tumour specific cDNA sequence SEQ ID 878.
XX	
KW	Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KV	immune response; prostate cancer; ss.
XX	
OS	Homo sapiens.
XX	
PN	MO300289747-A2.
XX	
PD	14-NOV-2002.
XX	
PF	09-MAY-2002; 2002WO-US014753.
XX	
PR	09-MAY-2001; 2001US-00852911.
PR	29-JUN-2001; 2001US-00895814.
XX	
PA	10-DEC-2001; 2001US-00012896.
XX	
XX	(CORI-) CORIXA CORP.
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI	Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI	Carter D, Li SX, Wang A, Skelky YAW, Hepner WT, Hurral J;
PI	Mcneill PD, Houghton RL, Vinals Y De Baasolsc, Foy TM, Matanabe Y;
PI	Deng T;
XX	
DR	WPI, 2003-167130/16.
XX	
PT	New prostate-specific proteins and genes, useful in gene therapy,
PT	paticularly for stimulating an immune response in a patient, or treating
PT	prostate cancer in a patient, as well as for diagnosing prostate cancer
PT	in a patient.

xx	Example 5; Page 617-618; 691pp; English.
xs	
cc	The present invention relates to novel prostate-specific proteins (PSP)
cc	and their coding sequences. The PSPs and their coding sequences are
cc	useful for stimulating an immune response in a patient, or for treating
cc	prostate cancer in a patient and for determining, detecting or diagnosing
cc	the presence of a cancer in a patient. The present sequence was used to
cc	illustrate the invention
xx	
SQ	Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
	Query Match 100.0%; Score 1017; DB 8; Length 1195;
	Best Local Similarity 100.0%; Pred. No. 2,6e-276;
	Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 ATGGAAGACAAAAAGACATCAAAACCMAAGAACACTTGGAAAATTAAAGCTTAGAGA 60
Dd	66 ATGGAAGACAAAAAGACATCAAAACCMAAGAACACTTGGAAAATTAAAGCTTAGAGA 125
Oy	61 AATTAGAAAGAAGCGAATTATTTGCATTAAGACAACGGAGAGACAGCATGCTAAAAAGA 120
Dd	126 AATTAGAAAGAAGCGAATTATTTGCATTAAGACAACGGAGAGACAGCATGCTAAAAAGA 185
Oy	121 CCTGTGCTTTTGCAATTTGACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
Dd	186 CCTGTGCTTTTGCAATTTGACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245
Oy	181 CTTAGACACACAGGAACCTCTTCCACAGTGGGCACTTGGCAATTTAAATAGCTGCTATT 240
Dd	246 CTTAGACACACAGGAACCTCTTCCACAGTGGGCACTTGGCAATTTAAATAGCTGCTATT 305
Oy	241 ATAGCATCTCGACTTTTCTTTACACTCTTCTGAGGAGAGTAATTCACCTTTAGCAACT 300
Dd	306 ATAGCATCTCGACTTTTCTTTACACTCTTCTGAGGAGAGTAATTCACCTTTAGCAACT 365
Oy	301 TCCCATCAACAATTTTTATAAAATTCCAATCCTGTGATCACAAAGTCTTGCCNATG 360
Dd	366 TCCCATCAACAATTTTTATAAAATTCCAATCCTGTGATCACAAAGTCTTGCCNATG 425
Oy	361 GTTTCGCATCACTCTCTTGGCAATTGGTTAACCTGCSAGGTGATAGCAGCAATTTGCCAA 420
Dd	426 GTTTCGCATCACTCTCTTGGCAATTGGTTAACCTGCSAGGTGATAGCAGCAATTTGCCAA 485
Oy	421 CTTGATATATGAAACCAAGTATTAAGAAAGTTTCCACATTGGTTGATPAAGTGATGTTAA 480
Dd	486 CTTGATATATGAAACCAAGTATTAAGAAAGTTTCCACATTGGTTGATPAAGTGATGTTAA 545
Oy	481 AGAAGAGAGTTGGGCTTCTCAGTTTCTTTTGGCTGTACTGCATGCAATTTATAGCTG 540
Dd	546 AGAAGAGAGTTGGGCTTCTCAGTTTCTTTTGGCTGTACTGCATGCAATTTATAGCTG 605
Oy	541 TCTTACCCAATGAGGCGATCTACAGATATACAGTTGCTTAAACTGGGCAATTCACAGGTC 600
Dd	606 TCTTACCCAATGAGGCGATCTACAGATATACAGTTGCTTAAACTGGGCAATTCACAGGTC 665
Oy	601 CAACAAAAATTAAGAAAGATGCTGATTTGAGCATATGTTTGGAGAAATGAGAGATTTATGTG 660
Dd	666 CAACAAAAATTAAGAAAGATGCTGATTTGAGCATATGTTTGGAGAAATGAGAGATTTATGTG 725
Oy	661 TCTCTGGGAATTTGGGGAATTGGCAATTAAGTGGCTGTGTTGGCTGGAATCTAATCCACT 720
Dd	726 TCTCTGGGAATTTGGGGAATTGGCAATTAAGTGGCTGTGTTGGCTGGAATCTAATCCACT 785
Oy	721 GTGAGTAGCTCTTTGACATGAGAGAAATTTCACTAATTCAGAGCAAGCTTAGAATTTGTT 780
Dd	786 GTGAGTAGCTCTTTGACATGAGAGAAATTTCACTAATTCAGAGCAAGCTTAGAATTTGTT 845
Oy	781 TTCCTTTACTGCGGCACAATATACAGCATATATTTTGGCTGGAATTAAGGATTAAGATATA 840
Dd	846 TTCCTTTACTGCGGCACAATATACAGCATATATTTTGGCTGGAATTAAGGATTAAGATATA 905
Oy	841 AAACAATTTTATAGTATACACCTCCAACTTTTATAGTATAGCTGTTTCTTCCAATTTGT 900

Db 906 AAAAATTTGTATGATACCTCCAACTTTATGATAGCTGTTTCTTCCAAATGTT 965
QY 901 GTCTGATATTTAAAGCACTATTTCTGCGCATGTTAGAGAAAGTACTGAAGATT 960
Db 966 GTCCGATATTTAAAGCACTATTTCTGCGCATGTTAGAGAAAGTACTGAAGATT 1025
QY 961 AGACATGTTGGAGAGAGCTGACCAAAATTAACAAAGTATGTTCCAGTTG 1017
Db 1026 AGACATGTTGGAGAGAGCTGACCAAAATTAACAAAGTATGTTCCAGTTG 1082

RESULT 12

ADB75572
ID ADB75572 strand; cDNA; 1195 BP.

AC ADB75572;

DT 04-DEC-2003 (first entry)

DE Prostate cancer marker cDNA.

KW Prostate; cancer; cytostatic; gene therapy; marker; ss.

OS Homo sapiens.

PN W02003009814-A2.

PD 06-FEB-2003.

PF 25-JUL-2002; 2002WO-US023913.

PR 25-JUL-2001; 2001US-0307982P.

PR 22-AUG-2001; 2001US-0314356P.

PR 25-SEP-2001; 2001US-0325020P.

PR 12-DEC-2001; 2001US-0341746P.

PR 05-MAR-2002; 2002US-0362158P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;

XX Hoersch S, Kamatkar S, Wonsey AM, Glatk K, Zhao X, Anderson D;

XX MPI; 2003-248033/24.

XX New nucleic acid molecule, useful for diagnosing or treating prostate

XX cancer.

XX Disclosure; SEQ ID NO 396; 99pp; English.

XX The invention relates to newly discovered cancer markers associated with

XX the cancerous state of prostate cells. Also disclosed is a method of

XX assessing whether a patient is afflicted with prostate cancer. The method

XX of the invention involves assessing whether a patient is afflicted with

XX prostate cancer by comparing the level of expression of a marker in a

XX patient sample and the normal level of expression of the marker in a

XX control non-prostate cancer sample, where a significant increase in the

XX level of expression of the marker in the patient sample and the normal

XX level indicates that the patient is afflicted with prostate cancer.

XX Nucleic acids of the invention are useful for diagnosing or treating

XX prostate cancer, and may be useful in gene therapy. Sequences given in

XX ADB75177-ADB7531 represent marker cDNA and proteins. Note: The sequence

XX data for this patent did not form part of the printed specification, but

XX was obtained in electronic format directly from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 1017; DB 10; Length 1195;

XX Best Local Similarity 100.0%; Pred. No. 2.6e-276;

XX Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAAGAGAGAAAGATCAACAACCAAGAAAGTCTTGAATAATGAAGCTTAGAGAGA 60

Db 66 ATGGAAGAGAGAGAAAGATCAACAACCAAGAAAGTCTTGAATAATGAAGCTTAGAGAGA 125
QY 61 AATTAGAAGAGAGATTAATTGATAGAAGACAGGGAGAGACCGAGCATGCTTAAGAA 120
Db 126 AATTAGAAGAGAGATTAATTGATAGAAGACAGGGAGAGACCGAGCATGCTTAAGAA 185
QY 121 CCTGTCTTTTGGCATTTTGGACCAACAGCCCATGCTGAATGAATTTGACTGCCCTTCAGAA 180
Db 186 CCTGTCTTTTGGCATTTTGGACCAACAGCCCATGCTGAATGAATTTGACTGCCCTTCAGAA 245
QY 181 CTTGAGACACACAGGAACTCTTCCACAGTGGCATTTGCCAATTAATTAATGCTGAT 240
Db 246 CTTGAGACACACAGGAACTCTTCCACAGTGGCATTTGCCAATTAATTAATGCTGAT 305
QY 241 ATAGCATCTGACCTTCTTCTTACACTCTTCCAGAGGAAATTAATCACTTTAGCACT 300
Db 306 ATAGCATCTGACCTTCTTCTTACACTCTTCCAGAGGAAATTAATCACTTTAGCACT 365
QY 301 TCCCATCAACAATATTTTAAATTCCAATCTGTCATCAACAAGTCTTGGCAATG 360
Db 366 TCCCATCAACAATATTTTAAATTCCAATCTGTCATCAACAAGTCTTGGCAATG 425
QY 361 GTTTCATCACTCTCTTGGCATTTGTTTACCTGCGAGGTTGATAGCAATTTGTCGA 420
Db 426 GTTTCATCACTCTCTTGGCATTTGTTTACCTGCGAGGTTGATAGCAATTTGTCGA 485
QY 421 CTTCAATTAAGAACCAAGTAAAGATTTGCAATGTTGTAATGAATGAATGAATGA 480
Db 486 CTTCAATTAAGAACCAAGTAAAGATTTGCAATGTTGTAATGAATGAATGAATGA 545
QY 481 AGAAAGCATTTGGGCTTCTCAGTTCTTTTGTGCTGATCTGATCAATTTAATGCTG 540
Db 546 AGAAAGCATTTGGGCTTCTCAGTTCTTTTGTGCTGATCTGATCAATTTAATGCTG 605
QY 541 TCTTACCCATGAGGAGATCTTCAAGATTAAGTGTCTTAATCTGGGCAATTAACAAGT 600
Db 606 TCTTACCCATGAGGAGATCTTCAAGATTAAGTGTCTTAATCTGGGCAATTAACAAGT 665
QY 601 CAACAAAATTAAGAAAGATGCTGATGAGATGATGTTGAGAAATGAGATTAATG 660
Db 666 CAACAAAATTAAGAAAGATGCTGATGAGATGATGTTGAGAAATGAGATTAATG 725
QY 661 TCTTGGGAATTTGGGATTTGGCAATTAATGCTGTTGGCTGTGATCATTTTCATCT 720
Db 726 TCTTGGGAATTTGGGATTTGGCAATTAATGCTGTTGGCTGTGATCATTTTCATCT 785
QY 721 GTGAGTACTCTTTGACATGAGAGATTTCACTATATTCAGAGCAAGCTAGGAATG 780
Db 786 GTGAGTACTCTTTGACATGAGAGATTTCACTATATTCAGAGCAAGCTAGGAATG 845
QY 781 TCCCTTCTACTGGGCAATTAACGATGATTTTGGCTGGAATTAAGATAGATATA 840
Db 846 TCCCTTCTACTGGGCAATTAACGATGATTTTGGCTGGAATTAAGATAGATATA 905
QY 841 AAAAATTTGTATGATACCTCCAACTTTATGATAGTGTGTTTCTTCCAAATGTT 900
Db 906 AAAAATTTGTATGATACCTCCAACTTTATGATAGTGTGTTTCTTCCAAATGTT 965
QY 901 GTCTGATATTTAAAGCACTATTTCTGCGCATGTTAGAGAAAGTACTGAAGATT 960
Db 966 GTCTGATATTTAAAGCACTATTTCTGCGCATGTTAGAGAAAGTACTGAAGATT 1025
QY 961 AGACATGTTGGAGAGAGCTGACCAAAATTAACAAAGTATGTTCCAGTTG 1017
Db 1026 AGACATGTTGGAGAGAGCTGACCAAAATTAACAAAGTATGTTCCAGTTG 1082

RESULT 13

ADB14328
ID ADB14328 strand; cDNA; 1195 BP.

XX ADB14328;

XX 18-DEC-2003 (first entry)
 DT Human prostate specific full length cDNA P789P.
 XX
 DE Human prostate specific full length cDNA P789P.
 XX
 KW Human; ser; prostate specific cDNA; cytostatic; immunostimulant;
 KW gene therapy; cell therapy; vaccine; T-cell epitope;
 KW class I major histocompatibility complex allele; MHC; prostate cancer;
 KM tumour; antigen presenting cell.
 XX
 OS Homo sapiens.
 XX
 PN US2003185830-A1.
 XX
 PD 02-OCT-2003.
 XX
 PF 12-NOV-2002; 2002US-00294025.
 XX
 PR 25-FEB-1997; 97US-00806099.
 PR 01-AUG-1997; 97US-00904804.
 PR 09-FEB-1998; 98US-00020956.
 PR 25-FEB-1998; 98US-00030607.
 PR 14-JUL-1998; 98US-00115453.
 PR 22-SEP-1998; 98US-00159812.
 PR 15-JAN-1999; 99US-00232149.
 PR 09-APR-1999; 99US-00288946.
 PR 13-JUL-1999; 99US-00352616.
 PR 12-NOV-1999; 99US-00439313.
 PR 18-NOV-1999; 99US-00443686.
 PR 14-JAN-2000; 2000US-00483672.
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00568100.
 PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605783.
 PR 09-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 02-OCT-2000; 2000US-00679426.
 PR 10-OCT-2000; 2000US-00685166.
 PR 09-NOV-2000; 2000US-00709729.
 PR 12-JAN-2001; 2001US-00759143.
 PR 09-FEB-2001; 2001US-00780669.
 PR 09-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-00895814.
 PR 10-DEC-2001; 2001US-00012896.
 PR 09-MAY-2002; 2002US-00144678.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Stolk JA, Kalos MD;
 XX
 DR WPI, 2003-756193/71.
 XX
 P-PSDB; ADB14329.
 XX
 PT New isolated polypeptide for use in a vaccine for stimulating an immune
 PT response, or for treating or diagnosis cancer, preferably prostate
 PT cancer.
 XX
 PS Example 5; Page: 101pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising no more than
 CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
 CC peptide comprises a fragment ADB13563 of that contain naturally processed
 CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
 CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific
 CC cDNA. One of 648 disclosed as new. Also included are nucleic acids
 CC encoding the proteins and peptides, expression vectors, a host cell
 CC transformed with the vector, an isolated antibody (or antigen binding
 CC fragment) that specifically binds to the protein or peptide, detecting
 CC the presence of a cancer in a patient (comprising contacting a patient
 CC sample with a binding agent that binds to the peptides or a polypeptide
 CC appearing as ADB13563, detecting the amount of polypeptide that binds to

CC the agent and comparing the amount of polypeptide to a predetermined cut-
 CC off value to determine the presence of cancer), a fusion protein
 CC comprising the peptide or proteins, stimulating or expanding T cells
 CC specific for a tumour protein comprising contacting T cells with the
 CC peptides or the isolated T cell population, treating prostate cancer in a
 CC patient comprising administering a composition comprising the peptides,
 CC nucleic acids, antibodies or compounds, determining the presence of a
 CC cancer in a patient and treating prostate cancer in a patient comprising
 CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
 CC from a patient with the peptide or antigen presenting cells that express
 CC (the peptides so that the T cells proliferate, and administering the
 CC proliferated T cells to the patient. The peptides (or an oligonucleotide
 CC that hybridises to nucleic acid encoding them), is used to detect the
 CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
 CC antigen-presenting cells expressing the nucleic acids, are used to
 CC stimulate or expand T cells specific for a tumour protein. The peptides,
 CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
 CC presenting cells are used to stimulate an immune response or treat
 CC prostate cancer in a patient. The present sequence is a known CDNA
 CC showing sequence similarity to one of the disclosed human prostate
 CC specific cDNAs. Note: Except where otherwise indicated, the sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030185830.
 XX
 SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1017; DB 10; Length 1195;
 Best Local Similarity 100.0%; Pred. No. 2,6e-276;
 Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGAAGCAGAAAGACATCAACCAAGAACTTGGAAATGAAGCTTAGAGAG 60
 DB 66 ATGGAAGCAGAAAGACATCAACCAAGAACTTGGAAATGAAGCTTAGAGAG 125
 QY 61 AATTGGAAGAAAGACATTAATTTGCTAAGAGACACGGAGAGACGATGCTTAAAGA 120
 DB 126 AATTGGAAGAAAGACATTAATTTGCTAAGAGACACGGAGAGACGATGCTTAAAGA 185
 QY 121 CCTGCGCTTTTCATTTGAGACCAAGCCATGCTGAAGATTGACCTGCTTACAGA 180
 DB 186 CCTGCGCTTTTCATTTGAGACCAAGCCATGCTGAAGATTGACCTGCTTACAGA 245
 QY 181 CTTGAGCAGACAGAGAACTTTTCCAGAGTGGACCTTSCAATTAATTAAGTGTATT 240
 DB 246 CTTGAGCAGACAGAGAACTTTTCCAGAGTGGACCTTSCAATTAATTAAGTGTATT 305
 QY 241 ATGACATCTGACTTTTCTTAACTCTTCTGAGGAGAAATTCACCTTTAGCACT 300
 DB 306 ATGACATCTGACTTTTCTTAACTCTTCTGAGGAGAAATTCACCTTTAGCACT 365
 QY 301 TCCCATCAACAATTTTATTAATAATTCATCTGCTGATCAACAAGTCTTGGCAATG 360
 DB 366 TCCCATCAACAATTTTATTAATAATTCATCTGCTGATCAACAAGTCTTGGCAATG 425
 QY 361 GTTTCATCACTCTGTTGGCATTTGTTACCGCCAGAGGTATGAGCAATTTGCCAA 420
 DB 426 GTTTCATCACTCTGTTGGCATTTGTTACCGCCAGAGGTATGAGCAATTTGCCAA 485
 QY 421 CTTCAATATGAGAACCAAGTATAGAAAGTTTCCAAATTTGGTATAGTATGTTAACA 480
 DB 486 CTTCAATATGAGAACCAAGTATAGAAAGTTTCCAAATTTGGTATAGTATGTTAACA 545
 QY 481 AGAAAGCAATTTGGGCTTCTGATTTCTTTTGTCTGATACGATGCAATTTATAGTCG 540
 DB 546 AGAAAGCAATTTGGGCTTCTGATTTCTTTTGTCTGATACGATGCAATTTATAGTCG 605
 QY 541 TCTTACCCATAGAGCGATCTTCAAGATACAAAGTTGTAATCTGGGCAATCAAGGTC 600
 DB 606 TCTTACCCATAGAGCGATCTTCAAGATACAAAGTTGTAATCTGGGCAATCAAGGTC 665
 QY 601 CAACAATAATGAAGATGCTGATGATGAGATGTTTGGAGATGAGAGATTTATGTG 660

RESULT 15

AAD62763
ID AAD62763 standard; DNA; 1195 BP.

XX
XX AAD62763;

XX
XX 12-FEB-2004 (first entry)

XX
XX Human STEAP (six transmembrane epithelial antigen of the prostate) DNA.

XX
XX Human; cancer; differential modulation; gene expression profile; STEAP;
XX six transmembrane epithelial antigen of the prostate; ds.

XX
XX Homo sapiens.

XX
XX PN US2003194733-A1.

XX
XX PD 16-OCT-2003.

XX
XX PF 21-MAR-2003; 2003US-00393567.

XX
XX PR 29-MAR-2002; 2002US-0368667P.

XX
XX PA (WANG/) WANG Y.

XX
XX PI Wang Y;

XX
XX DR MPI; 2003-844450/78.

XX
XX PT Diagnosing cancer comprises identifying differential modulation of each
XX PT gene (relative to the expression of the same genes in a normal
XX PT population) in a combination of genes.

XX
XX PS Claim 4; Page 54-55; Opp; English.

XX
XX CC The invention relates to a method for diagnosing cancer. The method
XX CC comprising identifying differential modulation of each gene (relative to
XX CC the expression of the same genes in a normal population) in a combination
XX CC of genes. The method, diagnostic portfolio and the kit are useful in
XX CC diagnosing cancer. The method may also be used for determining gene
XX CC expression profiles. The present sequence is human STEAP (six
XX CC transmembrane epithelial antigen of the prostate) DNA used to illustrate
XX CC the method of the invention

XX
XX SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1017; DB 10; Length 1195;

Best Local Similarity 100.0%; Pred. No. 2,6e-276;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGAAGCAGAAAAGACATCAACCAAGAACTTTGAAAAATGAAGCTTAGAGAG 60
DB 66 ATGGAAGCAGAAAAGACATCAACCAAGAACTTTGAAAAATGAAGCTTAGAGAG 125
QY 61 AATTAGAAGAGACGATTATTGATTAAGAGACCGGAGAGACGACATGCTAAAAAGA 120
DB 126 AATTAGAAGAGACGATTATTGATTAAGAGACCGGAGAGACGACATGCTAAAAAGA 185
QY 121 CCTGTCCTTTTGATTTGACCAACAGCCCATGCTGATGAATTTGACTGCCCTTGAGAA 180
DB 186 CCTGTCCTTTTGATTTGACCAACAGCCCATGCTGATGAATTTGACTGCCCTTGAGAA 245
QY 181 CTTGACGACACAGGAGACTTTTGCACAGTGACCTTGCAATTAATAATAGCTGCTATT 240
DB 246 CTTGACGACACAGGAGACTTTTGCACAGTGACCTTGCAATTAATAATAGCTGCTATT 305
QY 241 ATAGCATCTCTGACTTTTCTTTACACTCTTGTGAGGAGAAATTAATCAACCTTTAGCACT 300
DB 306 ATAGCATCTCTGACTTTTCTTTACACTCTTGTGAGGAGAAATTAATCAACCTTTAGCACT 365
QY 301 TCCCATCAACAATTTTATATAAATTCATCTCTGTCATCAACAAGCTTTGGCAATG 360
DB 366 TCCCATCAACAATTTTATATAAATTCATCTCTGTCATCAACAAGCTTTGGCAATG 425
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QY 361 GTTCCATCACTCTCTTGGCATTTGTTTACCTGCCAGGTGTGATAGAGCAATTTGCCAA 420
DB 426 GTTCCATCACTCTCTTGGCATTTGTTTACCTGCCAGGTGTGATAGAGCAATTTGCCAA 485
QY 421 CTTCAATTAAGAAACCAAGTATTAAGAACTTCCACTGTTGGATTAAGTGTATAC 480
DB 486 CTTCAATTAAGAAACCAAGTATTAAGAACTTCCACTGTTGGATTAAGTGTATAC 545
QY 481 AGAAGCAGTTGGGCTTCCAGTTCTTTTGTGCTGATGATCAATTTATAGCTG 540
DB 546 AGAAGCAGTTGGGCTTCCAGTTCTTTTGTGCTGATGATCAATTTATAGCTG 605
QY 541 TCTTACCAGTGGGAGATCTTACAGATCAAGTTGCTAACTGGGCATATCAACAGTCT 600
DB 606 TCTTACCAGTGGGAGATCTTACAGATCAAGTTGCTAACTGGGCATATCAACAGTCT 665
QY 601 CAACAAATTAAGAAAGATGCTGAGATTGAGCATGATGTTGGAGAAATGAGATTATG 660
DB 666 CAACAAATTAAGAAAGATGCTGAGATTGAGCATGATGTTGGAGAAATGAGATTATG 725
QY 661 TCTCTGGGAATTGTGGGATTGGCAATACAGGCTCTGTGGCTGTGACATCTATTCATCT 720
DB 726 TCTCTGGGAATTGTGGGATTGGCAATACAGGCTCTGTGGCTGTGACATCTATTCATCT 785
QY 721 GTGAGTGACTCTTTGACATGAGAGAAATTTCACTATATTCAAGCAAGCTAGGAATTTG 780
DB 786 GTGAGTGACTCTTTGACATGAGAGAAATTTCACTATATTCAAGCAAGCTAGGAATTTG 845
QY 781 TCCCTTCTACTGGGCAACAATACACGATGATTTTGGCTGGAATAAGTGTATATTA 840
DB 846 TCCCTTCTACTGGGCAACAATACACGATGATTTTGGCTGGAATAAGTGTATATTA 905
QY 841 AAAAATTTGTATGTATACCTCCACTTTATGATAGCTGTTTCTCTCCATTTGTT 900
DB 906 AAAAATTTGTATGTATACCTCCACTTTATGATAGCTGTTTCTCTCCATTTGTT 965
QY 901 GTTCGTATTTTAAAGCATATCTCTGCAATGCTTGAAGAAAGATGATGAATTT 960
DB 966 GTTCGTATTTTAAAGCATATCTCTGCAATGCTTGAAGAAAGATGATGAATTT 1025
QY 961 AGACATGTTGGGAGAGCTCAACAAATTAACAAACTGAGATATGTTCCAGTTG 1017
DB 1026 AGACATGTTGGGAGAGCTCAACAAATTAACAAACTGAGATATGTTCCAGTTG 1082
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Search completed: December 4, 2005, 21:08:44
Job time : 685.751 secs

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ORIGIN
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 100.0%; Score 1017; DB 6; Length 1193;
Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAAGCAGAAAAGACATCACAAACCAAGAACTTTGAAATGAAGCCTAGAGAGA 60
DB ATGGAAGCAGAAAAGACATCACAAACCAAGAACTTTGAAATGAAGCCTAGAGAGA 123
QY 61 AATTTGAAAGAACGATTTATTTGATTAAGGACACGGGAGAGACACAGATGCTTAAAGA 120
DB AATTTGAAAGAACGATTTATTTGATTAAGGACACGGGAGAGACACAGATGCTTAAAGA 183
QY 121 CCTGTGCTTTGATTTGACCAAAAGCCCATGCTGATGAATTTGACTGCCCTTGAGAA 180
DB CCTGTGCTTTGATTTGACCAAAAGCCCATGCTGATGAATTTGACTGCCCTTGAGAA 243
QY 181 CTTCAGACACACAGGAACCTCTTCCACAGTGGCACTTGCCTAAATTAATAGCTGCTATT 240
DB CTTCAGACACACAGGAACCTCTTCCACAGTGGCACTTGCCTAAATTAATAGCTGCTATT 303
QY 241 ATAGCATCTTGACTTTCTTTACACTCTTTCTGAGGGAATTAATCACTTTAGCAACT 300
DB ATAGCATCTCTGACTTTCTTTACACTCTTTCTGAGGGAATTAATCACTTTAGCAACT 363
QY 301 TCCCATCAACAATTTTATTAATAATTCGAATCTGGTCAATCAACAAAGCTTGGCAATG 360
DB TCCCATCAACAATTTTATTAATAATTCGAATCTGGTCAATCAACAAAGCTTGGCAATG 423
QY 361 GTTTCATCATCTCTTGGCATTTGTTTACCTGACAGGTGTGATAGCAGCAATTTGTCCA 420
DB GTTTCATCATCTCTTGGCATTTGTTTACCTGACAGGTGTGATAGCAGCAATTTGTCCA 483
QY 421 CTTCATTAATGGAACCAAGTATTAAGAACTTCCACATTTGGTGAATAGTGAATTAACA 480
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QY 481 AGAAGCAGTTTGGGCTTCTCAGTTTCTTTTGTGCTGATGATGCAATTTATAGTCTG 540
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DB TCTTACCAATGAGCGGATCTTAACAGATACAGTTGGTAACTGGGCATATCAACAGTCT 663
QY 601 CAACAATAATTAAGAAAGTCTGATTAAGAGATGATGTTGAGAAATGGAATTTATGTG 660
DB CAACAATAATTAAGAAAGTCTGATTAAGAGATGATGTTGAGAAATGGAATTTATGTG 723
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DB TCTCTGGGAATTTGGGAATTTGGCAATACCTGCTGTGGCTGTGACATATTTCCATCT 783
QY 721 GTGAGTGACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATTTG 780
DB GTGAGTGACTCTTTGACATGAGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATTTG 843
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QY 841 AAAACAATTTGTATGATACCTCAACTTTTATATAGCTGTCTTTCTTCCAAATTTGT 900
DB AAAACAATTTGTATGATACCTCAACTTTTATATAGCTGTCTTTCTTCCAAATTTGT 963
QY 901 GTCTCGATATTTAAAGCACTACTATTCTGCGCATGCTTGAAGAAAGATACGAAGATT 960
DB GTCTCGATATTTAAAGCACTACTATTCTGCGCATGCTTGAAGAAAGATACGAAGATT 1023
QY 961 AGACATGTTGGAGAGACGTACCAAAATTAACAAAATGAGATATGTTCCCAAGTTG 1017

Db 1024 AGACATGTTGGAGAGACGTACCAAAATTAACAAAATGAGATATGTTCCCAAGTTG 1080

RESULT 2
LOCUS AR617054 1193 bp DNA linear PAT 14-FEB-2005
DEFINITION Sequence 1 from patent US 6833438.
ACCESSION AR617054
VERSION AR617054.1 GI:59720558
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1193)
AUTHORS Afar,D.E., Hubert,R.S., Raitano,A.B., Saffran,D.C. and Mitchell,S.C.
TITLE Serpentine transmembrane antigens expressed in human cancers and uses thereof
JOURNAL Patent: US 6833438-A 1 21-DEC-2004;
Ageneys, Inc.; Santa Monica, CA
FEATURES
source 1..1193
location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 1017; DB 6; Length 1193;
Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAAGCAGAAAAGACATCACAAACCAAGAACTTTGAAATGAAGCCTAGAGAGA 60
DB ATGGAAGCAGAAAAGACATCACAAACCAAGAACTTTGAAATGAAGCCTAGAGAGA 123
QY 61 AATTTGAAAGAACGATTTATTTGATTAAGGACACGGGAGAGACACAGATGCTTAAAGA 120
DB AATTTGAAAGAACGATTTATTTGATTAAGGACACGGGAGAGACACAGATGCTTAAAGA 183
QY 121 CCTGTGCTTTGATTTGACCAAAAGCCCATGCTGATGAATTTGACTGCCCTTGAGAA 180
DB CCTGTGCTTTGATTTGACCAAAAGCCCATGCTGATGAATTTGACTGCCCTTGAGAA 243
QY 181 CTTCAGACACACAGGAACCTTTCACAGTGGCACTTGCCTAAATTAATAGCTGCTATT 240
DB CTTCAGACACACAGGAACCTTTCACAGTGGCACTTGCCTAAATTAATAGCTGCTATT 303
QY 241 ATAGCATCTTGACTTTCTTTACACTCTTTCTGAGGGAATTAATCACTTTAGCAACT 300
DB ATAGCATCTCTGACTTTCTTTACACTCTTTCTGAGGGAATTAATCACTTTAGCAACT 363
QY 301 TCCCATCAACAATTTTATTAATAATTCGAATCTGGTCAATCAACAAAGCTTGGCAATG 360
DB TCCCATCAACAATTTTATTAATAATTCGAATCTGGTCAATCAACAAAGCTTGGCAATG 423
QY 361 GTTTCATCATCTCTTGGCATTTGTTTACCTGACAGGTGTGATAGCAGCAATTTGTCCA 420
DB GTTTCATCATCTCTTGGCATTTGTTTACCTGACAGGTGTGATAGCAGCAATTTGTCCA 483
QY 421 CTTCATTAATGGAACCAAGTATTAAGAACTTCCACATTTGGTGAATAGTGAATTTAACA 480
DB CTTCATTAATGGAACCAAGTATTAAGAACTTCCACATTTGGTGAATAGTGAATTTAACA 543
QY 481 AGAAGCAGTTTGGGCTTCTCAGTTTCTTTTGTGCTGATGATGCAATTTATAGTCTG 540
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QY 541 TCTTACCAATGAGGCGATCTTAAGATTAACAAGTTGTAACTGGGCAATATCAACAGTCT 600
DB TCTTACCAATGAGGCGATCTTAAGATTAACAAGTTGTAACTGGGCAATATCAACAGTCT 663
QY 601 CAACAATAATTAAGAAAGTCTGATTAAGAGATGATGTTTGAAGAAATGAGATTTATGTG 660

Db 664 CAACAAAATAAAGAGATGCGCTGATGAGCATGATGTTGGAGATGAGATTTATGTC 723
Qy 661 TCTCTGGGAATTTGGGATTTGGCAATACTGCGCTGCTGGTGGTGAACATCTATTCCATCT 720
Db 724 TCTCTGGGAATTTGGGATTTGGCAATACTGCGCTGCTGGTGGTGAACATCTATTCCATCT 783
Qy 721 GTGAGTGAATCTTTGACATGAGAGAAATTTGACATATATTTGACAGCAAGCTAGAAATGTT 780
Db 784 GTGAGTGAATCTTTGACATGAGAGAAATTTGACATATATTTGACAGCAAGCTAGAAATGTT 843
Qy 781 TCCCTTTTACTGGGACATATACAGCATGATTTTGGCTGGGAATTAAGTGAATGATATTA 840
Db 844 TCCCTTTTACTGGGACATATACAGCATGATTTTGGCTGGGAATTAAGTGAATGATATTA 903
Qy 841 AAACAAATTTGATATGATATACAGCTTCAATCTTTTATGATAGCTGTTTCTTCCATTTGTT 900
Db 904 AAACAAATTTGATATGATATACAGCTTCAATCTTTTATGATAGCTGTTTCTTCCATTTGTT 963
Qy 901 GTCTGATATTTAAAGCATATCTATTCCTGCGCATGCTTGAAGAAAGATATCTGAAGATT 960
Db 964 GTCTGATATTTAAAGCATATCTATTCCTGCGCATGCTTGAAGAAAGATATCTGAAGATT 1023
Qy 961 AGACATGTTGGGAAGAGCTGACCAAAATTAACAAACTGAGATATGTTCCCAAGTTG 1017
Db 1024 AGACATGTTGGGAAGAGCTGACCAAAATTAACAAACTGAGATATGTTCCCAAGTTG 1080

RESULT 3
AX155243 1193 bp DNA linear PAT 22-JUN-2001
LOCUS AX155243
DEFINITION Sequence 1 from Patent WO0140276.
ACCESSION AX155243
VERSION AX155243.1 GI:14536707
KEYWORDS

SOURCE
ORGANISM Homo sapiens (human)

REFERENCE 1
AUTHORS Afari,D.E., Hubert,R.S., Raitano,A.B., Saffran,D.C., Mitchell,S.C.,
Fatis,M. and Jakobovits,A.
TITLE Serpentine transmembrane antigens expressed in human prostate
cancers and uses thereof
JOURNAL Patent: WO 0140276-A 1 07-JUN-2001;
urogenesys, Inc. (US)
FEATURES
Source Location/Qualifiers
1..1193
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
64..1083
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC42677.1"
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/translation="MESRKQITNOEELMKKPRNLBEDVLIHKDGETSMLEKPVLL
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RKQFGLSPFPAVLAHAIVSLSPYMRSRVYRKLMMAYQOVQONEDMAIEHDVWRMLT
VSLGIVGLALALAVTSLPSVSDSLTWEFHYIQLGIVSLILGTHALIFANMK
MIDIKQFVWYTPTFMIAVFLPIVLIFKSLIFPCIRKILKIRHGMEDVTINKITE
ICSQL"

ORIGIN

Query Match 100.0%; Score 1017; DB 6; Length 1193;
Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAAGCGAAGAAAGCATACCAAGAAAGAACTTTGGAAATGAAGCCATGAGAGA 60
Db 64 ATGGAAGCGAAGAAAGCATACCAAGAAAGAACTTTGGAAATGAAGCCATGAGAGA 123

Qy 61 AATTAGAGAGAGCATATTTGATAGAGACGCGGAGAGACACAGATGCTAAAAAGA 120
Db 124 AATTAGAGAGAGCATATTTGATAGAGACGCGGAGAGACACAGATGCTAAAAAGA 183
Qy 121 CCGTGGCTTTTGGATTTGGACCAAAACGCCATGCTGATGAATTTGACTGCCCTTCGAA 180
Db 184 CCGTGGCTTTTGGATTTGGACCAAAACGCCATGCTGATGAATTTGACTGCCCTTCGAA 243
Qy 181 CTTGAGACACACAGAACTCTTTCCACAGTGGCACTTGGCAATTAATAGCTGATTT 240
Db 244 CTTGAGACACACAGAACTCTTTCCACAGTGGCACTTGGCAATTAATAGCTGATTT 303
Qy 241 ATAGCATCTGACTTTTCTTTTACACTCTTTGAGGAGATTAATCACCTTTAGCACT 300
Db 304 ATAGCATCTGACTTTTCTTTTACACTCTTTGAGGAGATTAATCACCTTTAGCACT 363
Qy 301 TCCCATCAACAAATTTTATTAATTAATTCGAATCTGCTCATCAAAAGCTTGGCAATG 360
Db 364 TCCCATCAACAAATTTTATTAATTAATTCGAATCTGCTCATCAAAAGCTTGGCAATG 423
Qy 361 GTTTCATCACTCTTTGGCATGTTTACCTGCGCAGTGTGATAGAGCAATTTGCCAA 420
Db 424 GTTTCATCACTCTTTGGCATGTTTACCTGCGCAGTGTGATAGAGCAATTTGCCAA 483
Qy 421 CTTGATATGGAACCAAGATTAAGAGATTTCCATTTGTTGATTAAGTGAATTTAACA 480
Db 484 CTTGATATGGAACCAAGATTAAGAGATTTCCATTTGTTGATTAAGTGAATTTAACA 543
Qy 481 AGAAGAGATTTGGGCTTTCAGTTTCTTTTCTGCTGATGATGCAATTAATGATGCTG 540
Db 544 AGAAGAGATTTGGGCTTTCAGTTTCTTTTCTGCTGATGATGCAATTAATGATGCTG 603
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Db 664 CAACAAAATAAAGAGATGCGCTGATGAGCATGATGTTGGAGATGAGATTTATGTC 723
Qy 661 TCTCTGGGAATTTGGGATTTGGCAATACTGCGCTGCTGGTGGTGAACATCTATTCCATCT 720
Db 724 TCTCTGGGAATTTGGGATTTGGCAATACTGCGCTGCTGGTGGTGAACATCTATTCCATCT 783
Qy 721 GTGAGTGAATCTTTGACATGAGAGAAATTTGACATATATTTGACAGCAAGCTAGAAATGTT 780
Db 784 GTGAGTGAATCTTTGACATGAGAGAAATTTGACATATATTTGACAGCAAGCTAGAAATGTT 843
Qy 781 TCCCTTTTACTGGGACATATACAGCATGATTTTGGCTGGGAATTAAGTGAATGATATTA 840
Db 844 TCCCTTTTACTGGGACATATACAGCATGATTTTGGCTGGGAATTAAGTGAATGATATTA 903
Qy 841 AAACAAATTTGATATGATATACAGCTTCAATCTTTTATGATAGCTGTTTCTTCCATTTGTT 900
Db 904 AAACAAATTTGATATGATATACAGCTTCAATCTTTTATGATAGCTGTTTCTTCCATTTGTT 963
Qy 901 GTCTGATATTTAAAGCATATCTATTCCTGCGCATGCTTGAAGAAAGATATCTGAAGATT 960
Db 964 GTCTGATATTTAAAGCATATCTATTCCTGCGCATGCTTGAAGAAAGATATCTGAAGATT 1023
Qy 961 AGACATGTTGGGAAGAGCTGACCAAAATTAACAAACTGAGATATGTTCCCAAGTTG 1017
Db 1024 AGACATGTTGGGAAGAGCTGACCAAAATTAACAAACTGAGATATGTTCCCAAGTTG 1080

RESULT 4
CO776742 1195 bp DNA linear PAT 11-MAR-2004
LOCUS CO776742
DEFINITION Sequence 428 from Patent EP1394274.
ACCESSION CO776742
VERSION CO776742.1 GI:145380132
KEYWORDS Homo sapiens (human)

ORGANISM	REFERENCE
Homo sapiens	1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.	
	Ohnani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuahara, K. Methods of testing for bronchial asthma or chronic obstructive pulmonary disease Patent: EP 1394274-A 428 03-MAR-2004; Genex Research, Inc. (JP)
FEATURES	Location/Qualifiers
source	1..1195
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	/mol_type="unassigned DNA"
	/db_xref="taxon:9606"
ORIGIN	

Query Match	100.0%	Score 1017	DB 6	Length 1195
Best Local Similarity	100.0%	Pred. No. 2.6e-21		
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QY	1	ATGAAAGCAGAAAAGACATCACAAACCAAGAGAACTTTGGAAAAATGACCTAGAGAGA	60	
Db	66	ATGGAAACAGAAAAGACATCACAAACCAAGAGAACTTTGGAAAAATGACCTAGAGAGA	125	
QY	61	AATTTAGAAAGACGATTATTTGCTATAGGACACGGGAGACCGACATGCTTAAAAAGA	120	
Db	126	AATTTAGAAAGACGATTATTTGCTATAGGACACGGGAGAGACGACATGCTTAAAAAGA	185	
QY	121	CGTGGCTTTTGGCATTGTGACCAAAACAGCCCATGCTGATGTAATTTGAATGGCCCTTCAGAA	180	
Db	186	CGTGGCTTTTGGCATTGTGACCAAAACAGCCCATGCTGATGTAATTTGAATGGCCCTTCAGAA	245	
QY	181	CTTGAGCAGACACAGGAACTCTTTTCCACAGTGGCACTTGCCAATTTAAATAGCTGATTT	240	
Db	246	CTTGAGCAGACACAGGAACTCTTTTCCACAGTGGCACTTGCCAATTTAAATAGCTGATTT	305	
QY	241	ATAGCATCTTGACATTTTCTTTTACACTCTTCTGAGGAAAGTAAATTCACCCCTTTAGCACT	300	
Db	306	ATAGCATCTTGACATTTTCTTTTACACTCTTCTGAGGAAAGTAAATTCACCCCTTTAGCACT	365	
QY	301	TCCCATCAACAATATTTTATTAATAATTCCATCCGTGCATCAACAAAGTCTTGCCCAATG	360	
Db	366	TCCCATCAACAATATTTTATTAATAATTCCATCCGTGCATCAACAAAGTCTTGCCCAATG	425	
QY	361	GTTCGCATCACTCTCTTGGAATGGTTTAACTGCGCAGGTGTGATAGCAGCAATTTGTCCAA	420	
Db	426	GTTCGCATCACTCTCTTGGAATGGTTTAACTGCGCAGGTGTGATAGCAGCAATTTGTCCAA	485	
QY	421	CTTCATATAGGAACCAAGTATAGAAAGTTTCCACATGGTGTGGATTAAGTGAATGTTTACA	480	
Db	486	CTTCATATAGGAACCAAGTATAGAAAGTTTCCACATGGTGTGGATTAAGTGAATGTTTACA	545	
QY	481	AGAAAGCAGTTGGGCTTCTCAGTTTCTTTTGGCTGATCTGCATGCAATTTATAGTCTG	540	
Db	546	AGAAAGCAGTTGGGCTTCTCAGTTTCTTTTGGCTGATCTGCATGCAATTTATAGTCTG	605	
QY	541	TCTTAACCAATAGAGCCCATCTCTACAGATACAAAGTTTGCTAAACTGGGCATATCAACAGCTC	600	
Db	606	TCTTAACCAATAGAGCCCATCTCTACAGATACAAAGTTTGCTAAACTGGGCATATCAACAGCTC	665	
QY	601	CAACAAAATAAAGAAAGATGCTGGAATTAGCATGATGTTGGAGATAGGAAATTTATGTG	660	
Db	666	CAACAAAATAAAGAAAGATGCTGGAATTAGCATGATGTTGGAGATAGGAAATTTATGTG	725	
QY	661	TCTGTGGAAATTGGGATTGGCAATACCTGGCTCTGTTGGCTGTGACATCTATTTCACTCT	720	
Db	726	TCTGTGGAAATTGGGATTGGCAATACCTGGCTCTGTTGGCTGTGACATCTATTTCACTCT	785	
QY	721	GTGAGTCACTTTTGAACAATGAGAAATTTCACTATATTCAGACAAAGCTATGGAATTTGTT	780	
Db	786	GTGAGTCACTTTTGAACAATGAGAAATTTCACTATATTCAGACAAAGCTATGGAATTTGTT	845	

QY	781	TCCCTTCACAGGGGCAAAATACAGCAATGATTTTTCGTCGAATTAAGATATGATATA	840
Db	846	TCCCTTCACAGGGGCAAAATACAGCAATGATTTTTCGTCGAATTAAGATATGATATA	905
QY	841	AAACAATTTGTATGTATACACCTTCAACTTTTATGATAGCTGTTTTCTTCCAAATGTT	900
Db	906	AAACAATTTGTATGTATACACCTTCAACTTTTATGATAGCTGTTTTCTTCCAAATGTT	965
QY	901	GTCCTGATATTTAAAGACATCTATTTCTCGCACTGTTGAGAAAGATATCTGAACATT	960
Db	966	GTCCTGATATTTTAAAGACATCTATTTCTCGCACTGTTGAGAAAGATATCTGAACATT	1025
QY	961	AGACATGTTGGGAAGACGTCAACCAAAATTACAAACTAGATATGTTCCCAAGTTG	1017
Db	1026	AGACATGTTGGGAAGACGTCAACCAAAATTACAAACTAGATATGTTCCCAAGTTG	1082
RESULT 5			
LOCUS	AR366780	1195 bp	DNA
DEFINITION	Sequence 1 from patent US 6329503.	linear	PAT 12-SEP-2003
ACCESSION	AR366780		
VERSION	AR366780.1	GI:34599746	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1195)		
	Alfar, D.E., Hubert, R.S., Leong, K., Raitano, A.B., Saffran, D. C. and		
	Mitchell, S.C.		
TITLE	Seperitive transmembrane antigens expressed in human cancers and		
	uses thereof		
JOURNAL	Patent: US 6329503-A 1 11-DEC-2001;		
	Agensys, Inc.; Santa Monica, CA;		
	WOX;		
FEATURES			
source	Location/Qualifiers		
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	/mol_type="genomic DNA"		
ORIGIN			
	Query Match	100.0%; Score 1017; DB 6; Length 1195;	
	Best Local Similarity 100.0%; Pred. No. 2.6e-231;		
	Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	ATGAAAAGCAAAAGACATCACAAACCAAGAAACCTTTGGAAAATGAAGCCTAGAGA	60
Db	66	ATGAAAAGCAAAAGACATCACAAACCAAGAAACCTTTGGAAAATGAAGCCTAGAGA	125
QY	61	AATTAGAAAGAAGCAATTAATTTGTCATPAGAGACCGGAGAGACACAGATGCTPAAAGA	120
Db	126	AATTAGAAAGAAGCAATTAATTTGTCATPAGAGACCGGAGAGACACAGATGCTPAAAGA	185
QY	121	CTGTGCTTTTGGCAATTTGCAACCAACGCCCATGCTGATGAATTTGACCTCCCTCAGAA	180
Db	186	CTGTGCTTTTGGCAATTTGCAACCAACGCCCATGCTGATGAATTTGACCTCCCTCAGAA	245
QY	181	CTTAGAGACACACAGAACTCTTTCCACAGTGGCACTTGGCAATTAATAAGTCGATTT	240
Db	246	CTTAGAGACACACAGAACTCTTTCCACAGTGGCACTTGGCAATTAATAAGTCGATTT	305
QY	241	ATAGCATCTCGAATTTTCTTTACACCTCTCTGAGGAAATAATTCACCTTTAGCAACT	300
Db	306	ATAGCATCTCGAATTTTCTTTACACCTCTCTGAGGAAATAATTCACCTTTAGCAACT	365
QY	301	TCCCATCAACAATTTTTTATTAATAATTCATCTCGTCATCAACAAAGCTTTGCCAATG	360
Db	366	TCCCATCAACAATTTTTTATTAATAATTCATCTCGTCATCAACAAAGCTTTGCCAATG	425
QY	361	GTTTCATCACTCTCTTGGCAATGTTTACTCTGAGGTGATGATAGAGAAATTTGTCAA	420
Db	426	GTTTCATCACTCTCTTGGCAATGTTTACTCTGAGGTGATGATAGAGAAATTTGTCAA	485

QY 421 CTTATATATGAGAACCAAGTATAGAGATTGCCATTGGTTGAGTAAGTAGATTATACA 480
DB 486 CTTATATATGAGAACCAAGTATAGAGATTGCCATTGGTTGAGTAAGTAGATTATACA 545
QY 481 AGAAGAGATTGGGCTTCTCAGTTCTTTTGGTCTGATGCAATTTTATAGCTG 540
DB 546 AGAAGAGATTGGGCTTCTCAGTTCTTTTGGTCTGATGCAATTTTATAGCTG 605
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DB 786 GTGAGTACTCTTGAATGAGAGAAATTTCACTATATGAGAGCAAGTATGTT 845
QY 781 TCCCTTCTACTGGGCAATATACAGCATTTGATTTTCTGGATTAAGTATATATA 840
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QY 901 GTCTGATATTTAAAGCATACTATTCTGCAATGCTTGAAGAAAGATGAGATT 960
DB 966 GTCTGATATTTAAAGCATACTATTCTGCAATGCTTGAAGAAAGATGAGATT 1025
QY 961 AGACATGTTGGAGAGAGTCAACCAATTAACAAATGAGATGTTGCCAGTTG 1017
DB 1026 AGACATGTTGGAGAGAGTCAACCAATTAACAAATGAGATGTTGCCAGTTG 1082

RESULT 6
LOCUS AR405830 1195 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 878 from patent US 6630305.
ACCESSION AR405830
VERSION AR405830.1 GI:40154667
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1195)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kales,M.D., Fanger,G.R., Reiter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6630305-A 878 07-OCT-2003;
CORIXA Corporation; Seattle, WA;
MOX;
FEATURES
source 1. 1195
Location/Qualifiers
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 1017; DB 6; Length 1195;
Best local similarity 100.0%; Pred. No. 2.6e-231.
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAAGCAGAAAGACATCAAAACAGAGAACTTTGGAAAATGAAGCTTAGAGAG 60
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DB 66 ATGGAAGCAGAAAGACATCAAAACAGAGAACTTTGGAAAATGAAGCTTAGAGAG 125
QY 61 AATTGAGAGAGACATTAATTGATTAAGACACCGGAGAGACAGCATGTCTAAAAAGA 120
DB 126 AATTGAGAGAGACATTAATTGATTAAGACACCGGAGAGACAGCATGTCTAAAAAGA 185
QY 121 CTTGCTTTTGGATTGACCAACAGCCCATGCTGATGAAATTTGACCTTCCAGAA 180
DB 186 CTTGCTTTTGGATTGACCAACAGCCCATGCTGATGAAATTTGACCTTCCAGAA 245
QY 181 CTTGACACACACAGAGACCTTTTGCACAGTGCATTTGCCAATTAATAGTGTATT 240
DB 246 CTTGACACACACAGAGACCTTTTGCACAGTGCATTTGCCAATTAATAGTGTATT 305
QY 241 ATAGCATCTGCACTTTCTTTTCACTCTTCTGAGGAGATTAATCACTTTAGCAACT 300
DB 306 ATAGCATCTGCACTTTCTTTTCACTCTTCTGAGGAGATTAATCACTTTAGCAACT 365
QY 301 TCCCATCAACATATTTTATAAATTTCCATCTCTGTCATCAACAAAGCTTTGCCAATG 360
DB 366 TCCCATCAACATATTTTATAAATTTCCATCTCTGTCATCAACAAAGCTTTGCCAATG 425
QY 361 GTTTCATCACTCTCTTGGCATTTGTTTACCTGCGAGGTTGATPACAGCAATTTGCCA 420
DB 426 GTTTCATCACTCTCTTGGCATTTGTTTACCTGCGAGGTTGATPACAGCAATTTGCCA 485
QY 421 CTTATATATGAGAACCAAGTATAGAGATTTCCATTTGGTGGATTAAGTAGATTATACA 480
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QY 601 CAACAATAAAGAGAGATGCTGGATTGAGCATGATGTTGGAGAAATGAGATTTATG 660
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DB 726 TCTCTGGAGATTGGGATTTGGCAATCTGCTCTGTTGGCTGGATGATTTCCACT 785
QY 721 GTGAGTACTCTTGAATGAGAGAAATTTCACTATATGAGAGCAAGTATGTT 780
DB 786 GTGAGTACTCTTGAATGAGAGAAATTTCACTATATGAGAGCAAGTATGTT 845
QY 781 TCCCTTCTACTGGGCAATATACAGCATTTGATTTTCTGGATTAAGTATATATA 840
DB 846 TCCCTTCTACTGGGCAATATACAGCATTTGATTTTCTGGATTAAGTATATATA 905
QY 841 AAACATTTGTATGATATACACTCCCACTTTTATGATAGCTGTTTCCCTCAATGTT 900
DB 906 AAACATTTGTATGATATACACTCCCACTTTTATGATAGCTGTTTCCCTCAATGTT 965
QY 901 GTCTGATATTTAAAGCATACTATTCTGCAATGCTTGAAGAAAGATGAGATT 960
DB 966 GTCTGATATTTAAAGCATACTATTCTGCAATGCTTGAAGAAAGATGAGATT 1025
QY 961 AGACATGTTGGAGAGAGTCAACCAATTAACAAATGAGATGTTGCCAGTTG 1017
DB 1026 AGACATGTTGGAGAGAGTCAACCAATTAACAAATGAGATGTTGCCAGTTG 1082

RESULT 7
LOCUS AR564210 1195 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 878 from patent US 6759515.
ACCESSION AR564210
VERSION AR564210.1 GI:53979261

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1195)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedic, T.S., Carter, D., Li, S.X., Wang, A., Skelky, Y.A.W., Hepler, W.T., and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6759515-A 878 06-JUL-2004;
Corixa Corporation; Seattle, WA
FEATURES
source
1. 1195
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 1017; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGGAAGGAGAAAGACATCAAAACCAAGAACTTTGAAAATGAAGCTTAGAGAGA 60
66 ATGGAAGGAGAAAGACATCAAAACCAAGAACTTTGAAAATGAAGCTTAGAGAGA 125
61 AATTAGAAGAGAGATTAATTTGCAATAGAGACAGGAGAGACCGATGCTTAAAGAGA 120
126 AATTAGAAGAGAGATTAATTTGCAATAGAGACAGGAGAGACCGATGCTTAAAGAGA 185
121 CCGTGCTTTTGCATTTGGACCAACAGCCCATGCTGATGAATTTGACTGCCCTTCAAGA 180
186 CCGTGCTTTTGCATTTGGACCAACAGCCCATGCTGATGAATTTGACTGCCCTTCAAGA 245
181 CTTGACGACACACAGGAACTCTTTTCCACAGTGAGCACTTGGCAATTTAAATAGTCTATT 240
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241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGAGAAATTAACCCCTTAGCAACT 300
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Db 786 GTGAGTCACTCTTTGACATGAGAAATTTCACTAATTTCAAGACCAAGCTTAGAATTTGT 845
Qy 781 TCCCTTCTACTGGGACAAATACAGCATTTGTTTTGGCTTGAATTAAGTGATAGATTA 840
Db 846 TCCCTTCTACTGGGACAAATACAGCATTTGTTTTGGCTTGAATTAAGTGATAGATTA 905
Qy 841 AAACATTTGATGATATGATACAGCTTCCCACTTTTATGATGATGCTTTTCCCTCAATTGTT 900
Db 906 AAACATTTGATGATATGATACAGCTTCCCACTTTTATGATGATGCTTTTCCCTCAATTGTT 965
Qy 901 GTCCGATATTTTAAAGCATACTATTCCTGCCATGCTTGAAGAAAGATACGAGATT 960
Db 966 GTCCGATATTTTAAAGCATACTATTCCTGCCATGCTTGAAGAAAGATACGAGATT 1025
Qy 961 AGACATGTTGGGAAAGACGTCAACCAAAATTAACAAACTGATGATTTGCCAGTTG 1017
Db 1026 AGACATGTTGGGAAAGACGTCAACCAAAATTAACAAACTGATGATTTGCCAGTTG 1082
RESULT 8
ARS89196 1195 bp DNA linear PAT 15-DEC-2004
LOCUS Sequence 878 from patent US 6800746.
DEFINITION ARS89196
ACCESSION ARS89196
VERSION ARS89196.1 GI:56636093
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1195)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedic, T.S., Carter, D., Li, S.X., Wang, A., Skelky, Y.A.W., Hepler, W.T., and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6800746-A 878 05-OCT-2004;
Corixa Corporation; Seattle, WA
FEATURES
source
1. 1195
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 1017; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGGAAGGAGAAAGACATCAAAACCAAGAACTTTGAAAATGAAGCTTAGAGAGA 60
66 ATGGAAGGAGAAAGACATCAAAACCAAGAACTTTGAAAATGAAGCTTAGAGAGA 125
61 AATTAGAAGAGAGATTAATTTGCAATAGAGACAGGAGAGACCGATGCTTAAAGAGA 120
126 AATTAGAAGAGAGATTAATTTGCAATAGAGACAGGAGAGACCGATGCTTAAAGAGA 185
121 CCGTGCTTTTGCATTTGGACCAACAGCCCATGCTGATGAATTTGACTGCCCTTCAAGA 180
186 CCGTGCTTTTGCATTTGGACCAACAGCCCATGCTGATGAATTTGACTGCCCTTCAAGA 245
181 CTTGACGACACACAGGAACTCTTTTCCACAGTGAGCACTTGGCAATTTAAATAGTCTATT 240
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301 TCCCATCAACAATATTTTAAATAATTCGAATCTGTGATCAACAAGCTTTGCCAATG 360
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	Accession	Length	Source
Db	426 GTTTCATCATCTCTCTGGCAATGGTTTACCTGGCCAGAGTGTATAGCACAAATTGTC	485	
Qy	421 CTTTCATTAATGGAACCAAGTATTAAGAAATTTCCACATTTGGTGGATTAAGTATGTTACA	480	
Db	486 CTTTCATTAATGGAACCAAGTATTAAGAAATTTCCACATTTGGTGGATTAAGTATGTTACA	545	
Qy	481 AGAAAGCAATTTGGGCTTCAGTTTCTTTTTCGTGTACCTGATGCAATTTATATGCTCG	540	
Db	546 AGAAAGCAATTTGGGCTTCAGTTTCTTTTTCGTGTACCTGATGCAATTTATATGCTCG	605	
Qy	541 TCTTACCCCAATGAGGCGATCCTACAGATACAAGTTGCTTAACTGGGCATATCAACAGCTC	600	
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Qy	601 CAACAAATTAAGAAAGATGCTCGATTGGATGGATGATGTTTGGAGAATGGAGATTTATGTG	660	
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Qy	661 TCTTCGGGAATTTGGGGAATGGCAATACCTGCTCTGTTGGCTGTGACATATTCACATCT	720	
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Qy	721 GTGAGTGACTCTTTCACATGAGAGAAATTTCACTATATTCAGAGAACTGGAATTTGTT	780	
Db	786 GTGAGTGACTCTTTCACATGAGAGAAATTTCACTATATTCAGAGAACTGGAATTTGTT	845	
Qy	781 TCCCTTTCTACTGGGCAACAATACCCATTTGTTTGCCTGGAATTAAGTATAGATATA	840	
Db	846 TCCCTTTCTACTGGGCAACAATACCCATTTGTTTGCCTGGAATTAAGTATAGATATA	905	
Qy	841 AAACAATTTGTATGATATACCTCCCAACTTTTATGATAGCTGTTTCTCTCCAAATTTGT	900	
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Qy	901 GTCCGATATTTTAAAGCACTACTATTCTCTGCCATGCTTGAGGAAGAATACTGAAGTT	960	
Db	966 GTCCGATATTTTAAAGCACTACTATTCTCTGCCATGCTTGAGGAAGAATACTGAAGTT	1025	
Qy	961 AGACATGGTGGGAGAGCGTCAACCAAAATTTAACAAACCTGAGATATGTTCCCAAGTT	1017	
Db	1026 AGACATGGTGGGAGAGCGTCAACCAAAATTTAACAAACCTGAGATATGTTCCCAAGTT	1082	
RESULT 9	AR654075	1195 bp	DNA linear PAT 13-JUN-2005
LOCUS	AR654075		
DEFINITION	Sequence 1 from patent US 6887975.		
ACCESSION	AR654075		
VERSION	AR654075.1		GI:67584962
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1195)		
AUTHORS	Afari,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and Mitchell,S.C.		
TITLE	Peptides derived from STEAP1		
JOURNAL	Patent: US 6887975-A 1 03-MAY-2005;		
FEATURES	Agency, Inc.; Santa Monica, CA		
source	Location/Qualifiers		
	1..1195		
	/organism="Unknown"		
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Query Match	100.0%	Score 1017	DB 6	Length 1195
Best Local Similarity	100.0%	Pred. No. 2.6e-231		
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Db	66	ATGGAAACACAGAAAGACATCCAAACCAAGAACTTTGGAAATGAAGCTTAGAGAA	125	

QY	61	AATTAGAAAGAGATTAATTGATTAAGACACGGGAGAGACCGACATGCTAAAGA	120
Db	126	AATTTAGAAGAGAGATTAATTGATTAAGACACGGGAGAGACCGACATGCTAAAGA	185
QY	121	CCGTGCTTTTGGCATTTGGACCCAAACAGCCCATGCTGATGAATTTGACGCCCTTCAGAA	180
Db	186	CCGTGCTTTTGGCATTTGGACCCAAACAGCCCATGCTGATGAATTTGACGCCCTTCAGAA	245
QY	181	CTTGAGCACACAGAACTCTTTCACAGTGGCATTTGCCAATTAAATAGCTCTATT	240
Db	246	CTTGAGCACACAGAACTCTTTCACAGTGGCATTTGCCAATTAAATAGCTCTATT	305
QY	241	ATAGATCTCGACCTTTCTTTTACACTCTTCGAGGGAAGTAATCACCCCTTAGCACT	300
Db	306	ATAGATCTCGACCTTTCTTTTACACTCTTCGAGGGAAGTAATCACCCCTTAGCACT	365
QY	301	TCCCATCAACATATTTTATMAATTCCAATCCGTGCATCAACAAAGCTTGGCAATG	360
Db	366	TCCCATCAACATATTTTATMAATTCCAATCCGTGCATCAACAAAGCTTGGCAATG	425
QY	361	GTTTCGATCACTCTCTTGGCATTTGGTTTAACTGCCAGGTGTGATAGCAATGTCCAA	420
Db	426	GTTTCGATCACTCTCTTGGCATTTGGTTTAACTGCCAGGTGTGATAGCAATGTCCAA	485
QY	421	CTTCATTAATGGAACCAAGTATPAAGAGTTTCCAACTGGTTGGATPAAGTAGTTTACA	480
Db	486	CTTCATTAATGGAACCAAGTATPAAGAGTTTCCAACTGGTTGGATPAAGTAGTTTACA	545
QY	481	AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTGTGCTACTGCATGCATTAATTAAGTCTG	540
Db	546	AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTGTGCTACTGCATGCATTAATTAAGTCTG	605
QY	541	TCTTACCCAATGAGGCCATCTCTACAGATACAAATTGCTTAACTGGGCATATCAACAGTCTC	600
Db	606	TCTTACCCAATGAGGCCATCTCTACAGATACAAATTGCTTAACTGGGCATATCAACAGTCTC	665
QY	601	CAACAAATTAAGAAGATGCGCTGGATTTGAGCATGATGTTGGAGAAATGGAATTTATGTG	660
Db	666	CAACAAATTAAGAAGATGCGCTGGATTTGAGCATGATGTTGGAGAAATGGAATTTATGTG	725
QY	661	TCTCTGGAAATTTGTGGATTTGGCAATCTGGCTCTGTTTGGCTGTGACATCTATTTCCATCT	720
Db	726	TCTCTGGAAATTTGTGGATTTGGCAATCTGGCTCTGTTTGGCTGTGACATCTATTTCCATCT	785
QY	721	GTGAGTCACTCTTTGACATGAGAGAAATTTCACTAATTCAGACCAAGCTAGGAATGTT	780
Db	786	GTGAGTCACTCTTTGACATGAGAGAAATTTCACTAATTCAGACCAAGCTAGGAATGTT	845
QY	781	TCCCTTCACTGGGACAAATACAGGCATGATTTTTCCTGGAAATTAAGTAGATAGATATA	840
Db	846	TCCCTTCACTGGGACAAATACAGGCATGATTTTTCCTGGAAATTAAGTAGATAGATATA	905
QY	841	AAACAATTTGATGATATACACTCTCAACTTTTATGATAGCTGTCTTCTCCAAATGTT	900
Db	906	AAACAATTTGATGATATACACTCTCAACTTTTATGATAGCTGTCTTCTCCAAATGTT	965
QY	901	GTCTGATATTTAAAGCATATCTATTCCTGCGATGCTTGAAGAAAGATATCTGAAGATT	960
Db	966	GTCTGATATTTAAAGCATATCTATTCCTGCGATGCTTGAAGAAAGATATCTGAAGATT	1025
QY	961	AGAAATGTTGGGAAGACGTCAACCAAAATTAACAAACTGAGATATGTTCCCAATGG	1017
Db	1026	AGAAATGTTGGGAAGACGTCAACCAAAATTAACAAACTGAGATATGTTCCCAATGG	1082

RESULT 10			
LOCUS	AX201105	1195 bp	DNA
DEFINITION	Sequence 735 from Patent WO0151633.		linear
ACCESSION	AX201105		
VERSION	AX201105.1	GI:15390890	
KEYWORDS			

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Rether,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 735 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..1195
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 1017; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAAGCAGAAAAGACATCAAAACCAAGAACTTTGGAAAATGAGCTTAGAGA 60
DB 66 ATGGAAGCAGAAAAGACATCAAAACCAAGAACTTTGGAAAATGAGCTTAGAGA 125
QY 61 AATTGGAAGAAAGAGATTATTTGATAGAGACAGGGAGAGACAGCATGCTAAAAAGA 120
DB 126 AATTGGAAGAAAGAGATTATTTGATAGAGACAGGGAGAGACAGCATGCTAAAAAGA 185
QY 121 CCTGTCCTTTTGATTTGACCAACAGCCCATGCTGATTTGACTGCTCTTACAGA 180
DB 186 CCTGTCCTTTTGATTTGACCAACAGCCCATGCTGATTTGACTGCTCTTACAGA 245
QY 181 CTTCAGCACACAGAGAACTTTTCACAGTGGCACTTCCCAATTAAATAGCTGCTATT 240
DB 246 CTTCAGCACACAGAGAACTTTTCACAGTGGCACTTCCCAATTAAATAGCTGCTATT 305
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QY 301 TCCCATCAACAATATTTTATATAAATTCCAATCTGTCATCAACAAGCTTGGCAATG 360
DB 366 TCCCATCAACAATATTTTATATAAATTCCAATCTGTCATCAACAAGCTTGGCAATG 425
QY 361 GTTTCATCACTCTCTTGGCAATGTTTAACTGCGCAGGTGTAGACAGCAATTGTCCA 420
DB 426 GTTTCATCACTCTCTTGGCAATGTTTAACTGCGCAGGTGTAGACAGCAATTGTCCA 485
QY 421 CTTCATATAGAAACCAAGTAAAGAGTTTCCACATTTGGTGAATAGAGATTTAAACA 480
DB 486 CTTCATATAGAAACCAAGTAAAGAGTTTCCACATTTGGTGAATAGAGATTTAAACA 545
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DB 606 TCTTACCAATGAGGCGATCTTACAGATACAGATTCTTAACTGGGCAATCAACGCTG 665
QY 601 CAACAAATTAAGAAAGATGCTGGATTTGAGCAATGTTTGAATGAGATTTTGTG 660
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DB 786 GTGAGTGACTTTTGAATGAGAAATTTCAATATTTTCAAGCAAGCTTAGGAATTTGT 845
QY 781 TCCCTTACTGGGACAAATACAGCATTTATTTTCTGGATTAAGTGAATGATATA 840
DB 846 TCCCTTACTGGGACAAATACAGCATTTATTTTCTGGATTAAGTGAATGATATA 905
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DB 966 GTCCGATATTTTAAAGATATCTATTTCTGCGCATGCTTGAAGAAAGATATGAGATT 1025
QY 961 AGACATGTTGGGAAGAGCGTCAACCAAAATTAACAAATCTAGATATGTTCCCACTTG 1017
DB 1026 AGACATGTTGGGAAGAGCGTCAACCAAAATTAACAAATCTAGATATGTTCCCACTTG 1082
RESULT 11
AX267904 1195 bp DNA linear PAT 26-OCT-2001
LOCUS AX267904
DEFINITION Sequence 878 from Patent WO0173032.
ACCESSION AX267904
VERSION AX267904.1 GI:16516522
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Rether,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepner,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 878 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..1195
/organism="Homo sapiens"
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ORIGIN
Query Match 100.0%; Score 1017; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAAGCAGAAAAGACATCAAAACCAAGAACTTTGAAAATGAGCTTAGAGA 60
DB 66 ATGGAAGCAGAAAAGACATCAAAACCAAGAACTTTGAAAATGAGCTTAGAGA 125
QY 61 AATTGGAAGAAAGAGATTATTTGATAGAGACAGGGAGAGACAGCATGCTAAAAAGA 120
DB 126 AATTGGAAGAAAGAGATTATTTGATAGAGACAGGGAGAGACAGCATGCTAAAAAGA 185
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DB 246 CTTCAGCACACAGAGAACTTTTCACAGTGGCACTTCCCAATTAAATAGCTGCTATT 305
QY 241 ATAGCATCTCTGACTTTTCTTTACACTCTTTCGAGGAGAAATTCACCCCTTAGCAACT 300
DB 306 ATAGCATCTCTGACTTTTCTTTACACTCTTTCGAGGAGAAATTCACCCCTTAGCAACT 365
QY 301 TCCCATCAACAATATTTTATATAAATTCCAATCTGTCATCAACAAGCTTGGCAATG 360

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Qy 361 GTTTCATCATCTCTTGGCAATGGTTTACCTGCAAGTGTATAGAGCAATGTCAA 420
Db 426 GTTTCATCATCTCTTGGCAATGGTTTACCTGCAAGTGTATAGAGCAATGTCAA 485
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Db 786 GTGAGGACCTCTTGAATGAGAGAGAAATTTCAATATTCAGAGCAAGCTAGAGATTTG 845
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Db 906 AAACAATTTGTATGTATACCTCCAACTTTATGATGATGATGATGATGATGATGAT 965
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Qy 961 AGACATGTTGGGAGAGCTCACCAAAATTAACAAACTGAGATGTTCCAGTTG 1017
Db 1026 AGACATGTTGGGAGAGCTCACCAAAATTAACAAACTGAGATGTTCCAGTTG 1082

RESULT 12
AX926483 1195 bp DNA linear PAT 19-DEC-2003
LOCUS AX926483
DEFINITION Sequence 35 from Patent EP1355150.
ACCESSION AX926483
VERSION AX926483.1 GI:40246089
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Wang, Y.
TITLE Panel of nucleic acid sequences for cancer diagnosis
JOURNAL Patent: EP 1355150-A 35 22-OCT-2003;
Ortho-Clinical Diagnostics, Inc. (US)
FEATURES
source
1. 1195
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 100.0%; Score 1017; DB 6; Length 1195;

Best Local Similarity 100.0%; Pred. No. 2,6e-231;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 66 ATGGAAGCAGAAAGACATCAAAACCAAGAACTTTGGAAATGAAGCCTAGAGAGA 125
Qy 61 AATTTAGAAGACGATTAATTTGATTAAGAGACAGGAGAGACAGCATGCTAAAAAGA 120
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Qy 241 ATAGCATCTGACCTTTTCTTACATCTTCTGAGGAGAAATTAATCACTTTAGCAACT 300
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Qy 421 CTTCATATATGAACCAAGTATTAAGAGTTTCCATGTTGATTAAGTATGATTAACA 480
Db 486 CTTCATATATGAACCAAGTATTAAGAGTTTCCATGTTGATTAAGTATGATTAACA 545
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Db 966 GTCCGATATTTTAAAGCATATCTTCCGCCATGCTTGAAGAGAAATATCTGAAGATT 1025
Qy 961 AGACATGTTGGGAGAGCTCACCAAAATTAACAAACTGAGATGTTCCAGTTG 1017
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RESULT 13

AX951736 1195 bp DNA linear PAT 08-JAN-2004
LOCUS AX951736
DEFINITION Sequence 35 from Patent EP1367138.
ACCESSION AX951736
VERSION AX951736.1 GI:40782084
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Wang, Y.
TITLE Markers for breast cancer prognosis
JOURNAL Patent: EP 1367138-A 35 03-DEC-2003;
Ortho Clinical Diagnostics Inc. (US)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 100.0%; Score 1017; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAAGAGAAAAGACATCAACCAAGAAAGCTTGGAAATGAGCGCTAGAGAG 60
DB 66 ATGGAAGAGAAAAGACATCAACCAAGAAAGCTTGGAAATGAGCGCTAGAGAG 125
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DB 126 AATTAGAAGAAAGAGATTTATGATAGAGACAGGAGAGACAGCATGCTAAAGAA 185
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DB 186 CCGTGTCTTTTGCAATTTGCAACCAACAGCCCATGCTGATGAATTTGACGCCCTTCAGAA 245
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QY 781 TCCCTTCACTGGGACAAATACAGCATTAATTTTCCCTGAAATAGTGAATGATATA 840
DB 846 TCCCTTCACTGGGACAAATACAGCATTAATTTTCCCTGAAATAGTGAATGATATA 905
QY 841 AAACAATTTGTATGATATACACTCCAACTTTATGATAGCTGTTTCTTCCAAATGTT 900
DB 906 AAACAATTTGTATGATATACACTCCAACTTTATGATAGCTGTTTCTTCCAAATGTT 965
QY 901 GTCTGATATTTAAAGATATCTATTTCTGCAATGCTTGGAGAGAAAGATCTGAAGATT 960
DB 966 GTCTGATATTTAAAGATATCTATTTCTGCAATGCTTGGAGAGAAAGATCTGAAGATT 1025
QY 961 AGACATGTTGGGAAGACGTCAACCAAAATTAACAAACCTGAGATATGTTCCAGTTG 1017
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LOCUS AX960014
DEFINITION Sequence 35 from Patent EP1349104.
ACCESSION AX960014
VERSION AX960014.1 GI:40880240
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Jackoe, T.
TITLE Method of selecting a portfolio of markers for use in a diagnostic
JOURNAL application
Patent: EP 1349104-A 35 01-OCT-2003;
Ortho-Clinical Diagnostics, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAAGAGAAAAGACATCAACCAAGAAAGCTTGGAAATGAGCGCTAGAGAG 60
DB 66 ATGGAAGAGAAAAGACATCAACCAAGAAAGCTTGGAAATGAGCGCTAGAGAG 125
QY 61 AATTAGAAGAAAGAGATTTATGATAGAGACAGGAGAGACAGCATGCTAAAGAA 120
DB 126 AATTAGAAGAAAGAGATTTATGATAGAGACAGGAGAGACAGCATGCTAAAGAA 185
QY 121 CCGTGTCTTTTGCAATTTGCAACCAACAGCCCATGCTGATGAATTTGACGCCCTTCAGAA 180
DB 186 CCGTGTCTTTTGCAATTTGCAACCAACAGCCCATGCTGATGAATTTGACGCCCTTCAGAA 245
QY 181 CTTGAGCAGACAGAGAACTCTTCCAGAGTGGCACTTGGCAATTAATAGCTGCTATT 240
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Qy      421  |||||CTTCATATATGGAACCAAGTATTAAGAGTTTCCACATGTGTGATAGATGTAA 480
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LOCUS AF186249
DEFINITION Homo sapiens six transmembrane epithelial antigen of prostate (STEAP1) mRNA, complete cds.
ACCESSION AF186249
VERSION AF186249.1 GI:6572947
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1195)
Hubert, R.S., Vivanco, I., Chen, E., Rastegar, S., Leong, K., Jakobovits, A., Saffran, D.C. and Afar, D.E.
STEAP: a prostate-specific cell-surface antigen highly expressed in human prostate tumors
Proc. Natl. Acad. Sci. U.S.A. 96 (25), 14523-14528 (1999)
JOURNAL 2 (bases 1 to 1195)
PUBMED 10588738
HUBERT, R.S., VIVANCO, I., CHEN, E., RASTEGAR, S., LEONG, K., MITCHELL, S.C., MADRASWALA, R., ZHOU, Y., KUO, J., RAITANO, A.B., JAKOBOVITS, A., SAFFRAN, D.C. and AFAR, D.E.H.

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TITLE Direct Submission
JOURNAL Submitted (14-SEP-1999) UroGeneSys Inc., 1701 Colorado Ave., Santa Monica, CA 90404, USA
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ORIGIN
Query Match 100.0%; Score 1017; DB 8; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2,6e-231;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      366  |||||TCCCATCAACAATATTTTATAAATTCCAATCTCTGTCATCAACAAGCTTTGCCAAT 425
Qy      361  |||||GTTTCATCACTCTCTGGCATGTGTACTCGCAGGTGATAGACAAATGTCCAA 420
Db      426  |||||GTTTCATCACTCTCTGGCATGTGTACTCGCAGGTGATAGACAAATGTCCAA 485
Qy      421  |||||CTTCATATATGGAACCAAGTATTAAGAGTTTCCACATGTGTGATAGATGTAA 480
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Qy      481  |||||AGAAAGAGTTGGGCTTCTCAGTTCTTTTGTGCTGACTGCAATGCAATTTATGCTG 540
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Job time : 5380.03 secs

GenCore version 5.1.6
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(without alignments)
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Perfect score: 1017
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 segs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_est2.*
3: gb_est3.*
4: gb_hlc.*
5: gb_est4.*
6: gb_est5.*
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8: gb_est7.*
9: gb_gsa1.*
10: gb_gsa2.*
11: gb_gsa3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	904.6	88.9	1045	AY403219	AY403219 Pan trogl
3	776	76.3	884	CA488012	CA488012 AGENCCOURT
4	738.6	72.6	1050	AY403220	AY403220 Mus muscu
5	737	72.5	1211	AK010437	AK010437 Mus muscu
6	692.8	68.1	881	BG565247	BG565247 602582917
7	651	64.0	710	BB875216	BB875216 601488516
8	639.2	62.9	827	CV983083	CV983083 UMC-dmX
9	623	60.1	961	BG762026	BG762026 602718984
10	611.4	60.1	796	BG182296	BG182296 RST1161 A
11	605.4	59.5	720	CA446381	CA446381 UI-H-ED1-
12	598	58.8	609	CD677954	CD677954 h024h02.Y
13	598	58.8	697	DN997716	DN997716 TC115356
14	597.8	58.8	920	BB881257	BB881257 601492338
15	596	58.6	742	CK757709	CK757709 AGENCCOURT
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17	590	58.0	733	BI552907	BI552907 603197827
18	589.6	58.0	825	CK753134	CK753134 AGENCCOURT
19	586.2	57.6	609	BX103101	BX103101 BX103101
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ALIGNMENTS

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LOCUS
DEFINITION
AY403218 Homo sapiens STEAP gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION
AY403218.1 GI:39759201
VERSION
GSS.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1. (bases 1 to 1050)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCES
2 (bases 1 to 1050)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J., Adams,M.D. and Cargill,M.
Direct Submision
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1050
/gene="STEAP"
/locus_tag="HCM1484"
ORIGIN
Query Match 99.8%; Score 1015.4; DB 10; Length 1050;
Best Local Similarity 99.9%; Pred. No. 1.3e-259;
Matches 1016; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGGAAGAGAAAAGACATCAAAACCAAGAACTTTGAAAATGAAGCTTAGAGA 60
DB 31 ATGGAAGAGAAAAGACATCAAAACCAAGAACTTTGAAAATGAAGCTTAGAGA 90
QY 61 AATTGAAGAAAGACATTAATTTGCTAAGAGACACGGAGAGACCGACATGCTAAAAAGA 120
DB 91 AATTGAAGAAAGACATTAATTTGCTAAGAGACACGGAGAGACCGACATGCTAAAAAGA 150
QY 121 CCGTGCCTTTTGATTTGACCCAAACAGCCCATGCTGAATTTGACCTGCCTTGAGA 180
DB 151 CCGTGCCTTTTGATTTGACCCAAACAGCCCATGCTGAATTTGACCTGCCTTGAGA 210
QY 181 CTTGACAGACACAGGAACTCTTTCCACAGTGGCAGCTTGGCAATTAATAGCTGCTATT 240
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QY 301 TCCCATCAACAATTTTATAAATTTCCAACTCTGCTATCAACAAGCTTGGCAATG 360
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RESULT 2
AY403219
LOCUS

AY403219

1045 bp

DNA

linear

GSS 15-DEC-2003

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DEFINITION Pan trolodytes STEAP gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION AY403219
VERSION AY403219.1 GI:39759202
KEYWORDS GSS.
SOURCE Pan trolodytes (chimpanzee)
ORGANISM Pan trolodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.
REFERENCE 1 (bases 1 to 1045)
Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Infering nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1045)
Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment
FEATURES
source
1..1045
/organism="Pan trolodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1045
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/locus_tag="HCM1484"
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Best Local Similarity 89.2%; Pred. No. 4.8e-230;
Matches 907; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
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QY 61 AATTGAAGAAAGACATTAATTTGCTAAGAGACACGGAGAGACCGACATGCTAAAAAGA 120
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DB 146 CCGTGCCTTTTGATTTGACCCAAACAGCCCATGCTGAATTTGACTGCGCTTACAGA 205
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QY 361 GTTTCATCACTCTCTTGGCATTGTTTACCTGCAAGTGTGATAGCAGCAATTTGTC 420
DB 386 GTTTCATCACTCTCTTGGCATTGTTTACCTGCAAGTGTGATAGCAGCAATTTGTC 445
QY 421 CTTTCATTAATGGAACCAAGTAAAGAAAGTTTCCACATTTGTTGGATAATGATGTTA 480

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RESULT 4
AY403220
LOCUS
DEFINITION
MUS musculus STEAP gene, VIRUAL TRANSCRIPT, partial sequence.
ACCESSION
AY403220
VERSION
AY403220.1 GI:39759203
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1050)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
TITLE
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 1050)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
TITLE
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
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location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
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Best Local Similarity 82.9%; Pred. No. 9.9e-186;
Matches 843; Conservative 0; Mismatches 174; Indels 0; Gaps 0;
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QY 31 ATGGAATCAGTACGATGTTACAAACCCAGAACAACTTTGAAATGAAGCCAAAGGGA 90
DB |||||
QY 61 AATTGAAGAGAACGATTAATTGCAATAGAGACCGGAGAGCCAGCATGCTAAAGA 120
DB |||||
QY 91 AACCTGAAGATACAGTTACTGACTAAGAGACTCGGAGAGACGAGCATCTGAAGAAG 150
DB |||||
QY 121 CCTGTCTTTTGATTTGACCAAAAGCCCATGCTGATGAATTTAGCTGCCCTTCA 180
DB |||||
QY 151 CCGGGGCTCTCGACATTTGACGACGCGGCTCAGCTGATGCCCTTTAGCTGCCG 210
DB |||||
QY 181 CTTGACGACACAGAGAACTCTTTCCACAGTGGCACTTGGCAATTAATAGTGTCT 240
DB |||||
QY 211 CTTGACGACACAGAGAACTCTTTCCAAACCTGGCGCTTGGCAATGAAGTCGCTGC 270
DB |||||
QY 241 ATAGCATCTCTGATCTTTCTTTACATCTCTTGAAGGAAGTAATTCACCTTAGCA 300
DB |||||
QY 271 ATATCATCCCTGACTTTCCTGTCACACATTTGAGGAATCATCTACCCGTTAGT 330
DB |||||
QY 301 TCCCATCAACAATTTTATTAATTTCAATCTGCTGATCAACAAGCTTGGCAATG 360
DB |||||
QY 331 TCCCGTGAACATATTTTATTAATTTCAATCTGCTGATTTAAACAAGCTTGGCA 390
DB |||||
QY 361 GTTTCATCACTCTCTTGGCATGTGTACTGCGCAGGTGTGATGACAGCAATTTGCC 420

DB |||||
QY 391 GTGCGCATTAACCTCTTGGCAGCTGCTATTTGCCAGAGAGATTTGCGCAGTTGACG 450
DB |||||
QY 421 CTTCAATATGGAACCAAGTATAGAGTTTCCACATTTGGTGGATGAAGTATTAACA 480
DB |||||
QY 451 CTTGCAATGGAACCAAGTATAGAGTTTCCACATTTGGTGGATGAAGTATTAACA 510
DB |||||
QY 481 AGAAGCAGTTTGGGCTCTCAATTTCTTTTGTCTGATCTGATGCAATTTATAGTCTG 540
DB |||||
QY 511 AGAAGCAGTTTGGGCTCTCAATTTCTTTTGTCTGATCTGATGCAATTTATAGTCTG 570
DB |||||
QY 541 TCTTACCCATGAGGCGATCTTCAAGATTCATAGTGTCTTAACTGGGCAATTCACAG 600
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QY 571 TCATACCAATAGAGATCTTCAAGATTCATAGTGTCTTAACTGGGCAATTCACAG 630
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QY 601 CAACAAATTAAGAAAGATCTGATGATGATGATGATGATGATGATGATGATGATG 660
DB |||||
QY 631 CAACAAATTAAGAAAGATCTGATGATGATGATGATGATGATGATGATGATGATG 690
DB |||||
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DB |||||
QY 691 TCCCTGGGATTTGGGATTTGGCAATCTGCTGTTGGCTGATGATGATGATGATG 750
DB |||||
QY 721 GTGATGATCTTTTGAATGATGATGATGATGATGATGATGATGATGATGATG 780
DB |||||
QY 751 GTGAGGATCTTTTGAATGATGATGATGATGATGATGATGATGATGATGATG 810
DB |||||
QY 781 TCCCTTCTGAGGACCAATACAGCATGATTTTGGCTGATGATGATGATGATGAT 840
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DB |||||
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LOCUS
DEFINITION
AKO10437 1211 bp mRNA linear HNC 03-APR-2004
MUS musculus ES cells cDNA, RIKEN full-length enriched library, of
the prostate, full insert sequence.
ACCESSION
AKO10437
VERSION
AKO10437.1 GI:12845880
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
TITLE
JOURNAL
PUBMED
10349636
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
PUBMED
11042159
REFERENCE
2
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,

[illegible]

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98	ATGGAAGTACGTGACATGTATCAAAACCAAGAAAGAACTTTGGAAATATGAAACCAAGAGA	15			
61	AATTTGAAAGAGACATTTATTTGCATTAAGACACGGAGAGACACGATCTCTAAAAA	122			
158	AACCTGGAAGATACAGTACTCGACTTAAGGACTCGGAGAGAGACGAGCATCTAAAAA	217			
121	CGTGTGTTTTGATTTGACCAACAAACAGCCCATGCTAGTAATTTGACTGCCCTTCAAA	180			
218	CCGGGGCTCTCGCATTTGACAGACCGCGGTCCACGTCGATGCTTTGACTGCCCTCCGAG	277			
181	CTTCAGACACACAGGAACCTCTTTCACAGTGGACCTTGCCAAATTTAAATATGCTGTAAT	240			
278	CTTCAGACACGAGGAATTTCTTCCAAACGTGGCGCTTGCCAGTGAAGATGCTGCCATC	333			
241	ATAGCATCTCTGACTTTCTTTACACTCTCTGAGAGGAAGTAATTCACCTTTAGCACT	300			
338	ATATCATCCCTGACTTCTCTGACACACTTCTGAGGGAATATCATCTACCGTTAGTAAT	397			
301	TCCCATCAACAATATTTTATTAATAATTCGAATCTCGTGCATCAACAAAGCTTGGCAATG	360			
398	TCCCGTGAAACATATTTTATTAATAATTCGAATCTCGTGCATCAACAAAGCTTGGCAATG	455			
361	GTTCATCACTCTCTTGGCATTTGGTTAACTGCGAGGTGATGACAGCAATTTGCCAA	422			
458	GTGCGCATTAACCTCTTGGCATGCTGCTATTTTGCAGAGAGATTAAGCGCGAGTTGACAG	517			
421	CTTCATTAATGGAACCAAGTAATAAGATTTCCACTTGGTTGGATTAAGTGAATTTAA	480			
518	CTTCGAAATGGAACCAAGTAATAAGATTTCCCACTCGGTGTAAGATGATGATCTGGCC	577			
481	AGAAACAGTTGGGGCTTCTAGTTCTTTTGGTGAAGTCAAGCAATTTATAGCTG	540			
578	AGAAACAGTTGGGGCTTCTAGTTCTTTTGGTGAAGTCAAGCAATTTATAGCTG	637			
541	TCTTACCAATGAGGCGATCTCAAGATACAAAGTTGCTAAACTGGGCAATTCACAGGTC	600			
638	TCATACCAATGAGGCGATCTCAAGATACAAAGCTCAACTGAGGCTTCAACACAGTT	697			
601	CAACAAATAAAGAAAGATGCTCGATTTGAAGATGTTGGAAATAGAGATTTATGTC	666			
698	CAACAAATAAAGAAAGATGCTCGGTGTAGAGATATGCTGGAATAAGAGATTTATGTC	757			
661	TCTCTGGGAATTTGGGAAATGGCAATTAAGCTGCTGTTGGCTGTGACATCTATTCATCT	720			
758	TCCCTGGGAATTTGGGAGCTGGCAATCTTGGCTCTCTTGGCTGTGACATCTATTCATCT	817			
721	GTGAGTGAATCTTTTGAATGAGAGATTTCACTAATTTCAAGCAAGCTAGGAATTTT	780			
818	GTGAGGCAATCTTTTAACTCGAGAGAAATTTCACTAATTTCAAGCAAGCTAGGAATTTT	877			
781	TCCCTCTTAATGGGCAATACAGCATTAATTTTGGCTGGAATTAAGTGAATAGATATA	840			
878	TCTCTCTTCTGGGCAAGTACGCTTTGGTTTGGCTGGAATTAAGTGAATAGATGTC	937			

the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and Knaase H. After second strand synthesis, the double-stranded cDNAs were ligated to Sali adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life Technologies). The cDNAs were derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and Sali sites of the pCMV-Sport6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Preliminary library characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (-4.96-well plates) to confirm library quality (e.g. the presence of short polyA tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.) and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's bioinformatics group in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the director of the University of Missouri DNA Core facility at: bovine@net.missouri.edu. Citations: Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res. 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KW, Green JA, Forrester LJ, Springer GK, Didion BA, Mathalagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(A) tails. Biotechniques 31:38-42. Soares MB, MF Bonaldo, P Jelenko, L Su, L Lawton, A Efstathiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232. TAG_TISSUE=Conceptus-Corpus Luteum (mixed) TAG_SEQ=Not found"

ORIGIN

Query Match 62.9%; Score 639.2; DB 8; Length 827;
Best Local Similarity 90.2%; Pred. No. 3.2e-159;
Matches 683; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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301 TCCCATCAACAATTTTAAATTTCAATCTGGTCAATCAACAAGCTTTGCCAATG 360
|||||
371 TCCCATCAACAATTTTAAATTTCAATCTGGTCAATCAACAAGCTTTGCCAATG 430

QY 361 GTTTCATCACTCTCTTGATGATGTTTAACTCGCAGGTGATAGCAGCAATTTGCCAA 420
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DB 431 GTTTCATCACTCTCTTGATGATGTTTAACTCGCAGGTGATAGCAGCAATTTGCCAA 490
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QY 421 CTTGATTAATGAGAACCAAGATTAAGAACTTTTCCACATTTGATGATTAAGTGAATTAACA 480
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DB 491 CTTGATTAATGAGAACCAAGATTAAGAACTTTTCCACATTTGATGATTAAGTGAATTAACA 550
|||||
QY 481 AGAAGAGATTTGGGCTTTCCAGTTCTTTTGGCTGATGATGATGATTAAGTGAATTTAGTCTG 540
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QY 541 TCTTACCAATGAGAGCAGCTCTTACAGATTAAGTGAATTTAGTGAATTTAGTGAATTTAGTGA 600
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DB 671 CAACAAATTAAGAAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 730
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DB 731 TCTCTGGAATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGAT 790
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QY 721 GTGAGTGAATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGAT 757
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DB 791 GTGAGTGAATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGAT 827
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RESULT 9
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LOCUS
DEFINITION
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ACCESSION
BG762026
VERSION
BG762026.1 GI:14072679
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 (bases 1 to 961)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1713 row: h column: 21
High quality sequence stop: 750.
Location/Qualifiers
1..961
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4858820"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 49"
/note="Organ: skin; Vector: pOT7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)

FEATURES

source

ORIGIN

using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library. | "

Query Match 61.3%; Score 623; DB 2; Length 961;
Best Local Similarity 93.1%; Pred. No. 7e-155;
Matches 710; Conservative 0; Mismatches 40; Indels 13; Gaps 5;

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QY 1 ATGGAAGCAGAAAGACATCAACCAAGAAAGAACTTGGAAATGAAGCCCTAGAGA 60
DB 122 ATGGAAGCAGAAAGACATCAACCAAGAAAGAAATTTGGAAATGAAGCCCTAGAGA 181
QY 61 AATTAGAAGAAAGACATTAATTTGCATTAAGACACGGGAGAGACCAGCATGCTAAAAA 120
DB 182 AATTAGAAGAAAGACATTAATTTGCATTAAGACACGGGAGAGACCAGCATGCTAAAAA 241
QY 121 CCTGTGCTTTTGCATTTTGCACCAACAGCCCATGATGAATTTGACTGCTTCAGAA 180
DB 242 CCTGTGCTTTTGCATTTTGCACCAACAGCCCATGATGAATTTGACTGCTTCAGAA 301
QY 181 CTTGAGACACAGCAAGCACTTTCCACAGTGACATGCCAATTAATTAATGCTGCTATT 240
DB 302 CTTGAGACACAGCAAGCACTTTCCACAGTGACATGCCAATTAATTAATGCTGCTATT 361
QY 241 ATAGCATCTGCACTTTCTTTTACACTCTTCTGAGGAAAGTAATTCACCCCTTAGCACT 300
DB 362 ATGCAATCTGCACTTTCTTTTACACTCTTCTGAGGAAAGTAATTCACCCCTTAGCACT 421
QY 301 TCCCATCAACAAATATTTTAAATTAATTCATCTGCTCATCAACAAAGCTTCCCAATG 360
DB 422 TCCCATCAACAAATATTTTAAATTAATTCATCTGCTCATCAACAAAGCTTCCCAATG 481
QY 361 GTTTCATCACTCTCTTGGCAATGCTTACCTGCACTGATGATGAGAGCAATTTGCTCAA 420
DB 482 GTTTCATCACTCTCTTGGCAATGCTTACCTGCACTGATGATGAGAGCAATTTGCTCAA 541
QY 421 CTTCAATATGGAACCAAGTATTAAGAAAGTTTCCACATGTTGATTAAGTGAATTTTACA 480
DB 542 GTTCAATATGGAACCAAGTATTAAGAAAGTTTCCACATGTTGATTAAGTGAATTTTACA 601
QY 481 AGAAAGCAGTTTGGGCTTCTCAAGTTCTTTTGTCTGATGCAATGCAATTAATGCTG 540
DB 602 AGAAAGCAGTTTGGGCTTCTCAAGTTCTTTTGTCTGATGCAATTAATGCTG 660
QY 541 TCTTACCCATGAGGCGATCTTACAGATTAAGTGAATTTGAGGATTTCAACAGCTC 600
DB 661 TCTTACCCATGAGGCGATCTTACAGATTAAGTGAATTTGAGGATTTCAACAGCTC 720
QY 601 CAACAATAAAGAGATGCTGATGATGAGATGATGTTGGAGAAAT--GAGATTTATG 658
DB 721 CAACAATAAAGAGATGCTGATGATGAGATGATGTTGGAGAAATGCGCACTTATG 780
QY 659 TGTCTCTGGGAATTTGGGATTTGGC-----ATACTGCTCTGTTGGC--TGTCAT 709
DB 781 TGTCTCTGGGAGCTTTGTTGGCGAGCGGGGCAACCTTGGGCTGTTGGCTGTTGACAT 840
QY 710 CTATTCATCTGTGA--GTGACTCTTTGACATGAGAGAAATTTTC 751
DB 841 CTATTCATCTGTGACGTGACCTTTGACCTTGGGAGAAATTTTC 883

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RESULT 10

BG182296

LOCUS BG182296 796 bp mRNA linear EST 21-Apr-2001

DEFINITION RST1161 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG182296.1 GI:13703983

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE

Hominidae; Homo.
1 (bases 1 to 796)

AUTHORS

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramchandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,
Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cochren, K., Lo, K.,
Offenbacher, J., Danzig, J., and Ducar, M.

TITLE

Creation of genome-wide protein expression libraries using random
activation of gene expression

JOURNAL

Nat. Biotechnol. 19 (5), 440-445 (2001)

PUBMED

11329013

COMMENT

Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com

FEATURES

High quality sequence stop: 505.
Location/Qualifiers

SOURCE

1. 796
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 60.1%; Score 611.4; DB 2; Length 796;
Best Local Similarity 97.2%; Pred. No. 8.3e-152;
Matches 632; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

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QY 1 ATGGAAGCAGAAAGACATCAACCAAGAAAGAACTTGGAAATGAAGCCCTAGAGA 60
DB 147 ATGGAAGCAGAAAGACATCAACCAAGAAAGAAATTTGGAAATGAAGCCCTAGAGA 206
QY 61 AATTAGAAGAAAGACATTAATTTGCATTAAGACACGGGAGAGACCAGCATGCTAAAAA 120
DB 207 AATTAGAAGAAAGACATTAATTTGCATTAAGACACGGGAGAGACCAGCATGCTAAAAA 286
QY 121 CCTGTGCTTTTGCATTTTGCACCAACAGCCCATGATGAATTTGATGCTGCTTACGA 180
DB 267 CCTGTGCTTTTGCATTTTGCACCAACAGCCCATGATGAATTTGATGCTGCTTACGA 326
QY 181 CTTGAGACACAGCAAGCACTTTCCACAGTGACATGCCAATTAATTAATGCTGCTATT 240
DB 327 CTTGAGACACAGCAAGCACTTTCCACAGTGACATGCCAATTAATTAATGCTGCTATT 386
QY 241 ATAGCATCTGCACTTTCTTTTACACTCTTCTGAGGAAAGTAATTCACCCCTTAGCACT 300
DB 387 ATAGCATCTGCACTTTCTTTTACACTCTTCTGAGGAAAGTAATTCACCCCTTAGCACT 446
QY 301 TCCCATCAACAAATATTTTAAATTAATTCATCTGCTCATCAACAAAGCTTCCCAATG 360
DB 447 TCCCATCAACAAATATTTTAAATTAATTCATCTGCTCATCAACAAAGCTTCCCAATG 506
QY 361 GTTTCATCACTCTCTTGGCAATGCTTACCTGCACTGATGATGAGAGCAATTTGCTCAA 420
DB 507 GTTTCATCACTCTCTTGGCAATGCTTACCTGCACTGATGATGAGAGCAATTTGCTCAA 566
QY 421 CTTCAATATGGAACCAAGTATTAAGAAAGTTTCCACATGTTGATTAAGTGAATTTTACA 480
DB 567 CTTCAATATGGAACCAAGTATTAAGAAAGTTTCCACATGTTGATTAAGTGAATTTTACA 626
QY 481 AGAAAGCAGTTTGGGCTTCTCAAGTTCTTTTGTCTGATGCAATTAATTAATGCTG 540
DB 627 AGAAAGCAGTTTGGGCTTCTCAAGTTCTTTTGTCTGATGCAATTAATTAATGCTG 686

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QY 541 TCTTACCCATGAGCGGATCTTACAGATACAGTTGCTTAACTGGGCATATCAACAGGTC 600
|||||
DB 687 TCTTAGCATGAGGAGGATCTCTACAGATCAAGTTCTTAACTGGGCATATCAACAGGTC 746
QY 601 CAACAATAAAGAAAGATGCTGGATTTGAGCATGATGTTTGAGGAATGGA 650
|||||
DB 747 CAAC-AATAAAGAAAGATGCTGGATTTGAGCATGATGTTTGAGGAATGGA 795

RESULT 11
CA446381/c 720 bp mRNA linear EST 08-NOV-2002
LOCUS UI-H-ED1-axr-o-23-0-UI.s1 NCI CGAP ED1 Homo sapiens cDNA clone
DEFINITION UI-H-ED1-axr-o-23-0-UI 3', mRNA sequence.
ACCESSION CA446381
VERSION CA446381.1 GI:24810801
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 720)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbcr@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES

source Location/Qualifiers
1..720
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-ED1-axr-o-23-0-UI"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP ED1"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site 1: Bcl I;
Site 2: Not I; NCI CGAP ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C55. The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG TISSUE=chondrosarcoma
TAG LIB=UI-H-ED1
TAG_SEQ=CCTCAAGGCT"

ORIGIN

Query Match 59.5%; Score 605.4; DB 6; Length 720;
Best Local Similarity 99.8%; Pred. No. 3.3e-150;
Matches 606; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 411 AATTGCCAATTCATTAATGGAACAAGTATAGAAAGTTCCCATTTGGATAGAG 470
|||||
DB 720 AATTGCCAATTCATTAATGGAACAAGTATAGAAAGTTCCCATTTGGATAGAG 661

QY 471 GATGTTAACAGAAAGAGAGTTGGGCTTCTCAGTTCTTTTGTGTTGATGATGCAAT 530
|||||
DB 660 GATGTTAACAGAAAGAGAGCTGCGGCTTCTCAGTTCTTTTGTGTTGATGATGCAAT 601
QY 531 TTATAGTCGTGCTTCCCAATGAGCGAATCCATACAGATACAGAGTCTTAACTGGGCAT 590
|||||
DB 600 TTATAGTCGTGCTTCCCAATGAGCGAATCCATACAGATACAGAGTCTTAACTGGGCAT 541
QY 591 TCACAGAGTCCACAAATAAAGAAAGATGCTCGATGATGATGATGTTGGAGAAATGA 650
|||||
DB 540 TCACAGAGTCCACAAATAAAGAAAGATGCTCGATGATGATGATGTTGGAGAAATGA 481
QY 651 GATTTATGTCCTCTGGGAATTTGGAGATTTGGCAATCTGCTCTGTTGGCTGTGACATC 710
|||||
DB 480 GATTTATGTCCTCTGGGAATTTGGAGATTTGGCAATCTGCTCTGTTGGCTGTGACATC 421
QY 711 TATTCATCTGAGAGTACTCTTTCACATGAGAGAAATTTCACTATATTCAGAGCAAGCT 770
|||||
DB 420 TATTCATCTGAGAGTACTCTTTCACATGAGAGAAATTTCACTATATTCAGAGCAAGCT 361
QY 771 AGGAATGTTTCCCTTCTACTGAGCAATACAGCATTTGATTTGGCTGGAAATAGTG 830
|||||
DB 360 AGGAATGTTTCCCTTCTACTGAGCAATACAGCATTTGATTTGGCTGGAAATAGTG 301
QY 831 GATGATATTAACAATTGTAATGATACCTCCAACTTTATGATAGCTGTTTCT 890
|||||
DB 300 GATGATATTAACAATTGTAATGATACCTCCAACTTTATGATAGCTGTTTCT 241
QY 891 TCCAAATGTTGCCGATATTTTAAAGCACTATTTCCGATGCTGGAGAGAGAT 950
|||||
DB 240 TCCAAATGTTGCCGATATTTTAAAGCACTATTTCCGATGCTGGAGAGAGAT 181
QY 951 ACTGAAGATTACACATGTTGGGAAGACGTCAACAAATTAAACAACTGATATGTTTC 1010
|||||
DB 180 ACTGAAGATTACACATGTTGGGAAGACGTCAACAAATTAAACAACTGATATGTTTC 121
QY 1011 CCAAGTTG 1017
|||||
DB 120 CCAAGTTG 114

RESULT 12
CD677954 609 bp mRNA linear EST 24-JUN-2003
LOCUS ho24h02.y1 Human Trabecular meshwork cDNA: hohpbg Homo sapiens cDNA
DEFINITION ho24h02.y1 Human Trabecular meshwork cDNA: hohpbg Homo sapiens cDNA
clone ho24h02 5', mRNA sequence.
ACCESSION CD677954
VERSION CD677954.1 GI:32179685
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 609)
Tomarev,S.I., Wistow,G., Raymond,V., Dubois,S. and Maljukova,I.
Gene expression profile of the human trabecular meshwork: NEIBank
sequence tag analysis
Invest. Ophthalmol. Vis. Sci. 44 (6), 2588-2596 (2003)
JOURNAL PUBLISHED
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 24 row: h column: 02
Seq primer: M13Rp1 reverse primer (ABI).

FEATURES

source Location/Qualifiers
1..609
/organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="h024h02"
/tissue_type="Trabecular meshwork"
/dev_stage="adult"
/lab_host="EMD10B"
/clone_lib="Human Trabecular meshwork cDNA: h024h02"
/notes="Organ: Eye; Vector: pSPORT1; The cDNA, directionally cloned in the pSPORT1 vector (Life Technologies, Rockville, MD), was constructed at Bioserve Biotechnology (Laurel, MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). Sublibraries (designated ho, hp, and hq) were made from the first three 35-nt fractions of cDNA from a Sephacryl S-500 HR resin column. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

```

ORIGIN

Query Match 58.8%; Score 598; DB 6; Length 609;
 Best Local Similarity 99.8%; Pred. No. 3e-148;
 Matches 609; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 189 CACACAGAACTCTTCCACAGTGGCACTTCCAAATTAATAGCTGATTAATGATC 248
DB 1 CACACAGAACTCTTCCACAGTGGCACTTCCAAATTAATAGCTGATTAATGATC 59
QY 249 TCTGACTTTCTTTTACACTCTTCTGAGGGAATTAATCACTTTCAGCACTCCATCA 308
DB 60 TCTGACTTTCTTTTACACTCTTCTGAGGGAATTAATCACTTTCAGCACTCCATCA 119
QY 309 ACAATATTTTAAATTAATCCATCCGTCATCAACAAAGCTTGGCAATGGTTCCAT 368
DB 120 ACAATATTTTAAATTAATCCATCCGTCATCAACAAAGCTTGGCAATGGTTCCAT 179
QY 369 CACTCTCTTGGCAATGGTTTACCTGCAAGTGTGATAGCAGCAATGTCCCACTTCA 428
DB 180 CACTCTCTTGGCAATGGTTTACCTGCAAGTGTGATAGCAGCAATGTCCCACTTCA 239
QY 429 TGGACCAAGTATTAAGAGTTTCCACTGTTGATTAAGTGAATGTTAAAGAAAGCA 488
DB 240 TGGACCAAGTATTAAGAGTTTCCACTGTTGATTAAGTGAATGTTAAAGAAAGCA 299
QY 489 GTTTGGGCTTCTAGTTCTTTTGTGCTGACATGCAATTAATAGTGTCTTACC 548
DB 300 GTTTGGGCTTCTAGTTCTTTTGTGCTGACATGCAATTAATAGTGTCTTACC 359
QY 549 AATGAGCGCATCTTACAGATACAAAGTTGCTAACTGGGCAATCAACAGTCCACAAA 608
DB 360 AATGAGCGCATCTTACAGATACAAAGTTGCTAACTGGGCAATCAACAGTCCACAAA 419
QY 609 TAAAGAAATGCTGATGATGATGTTGAGAAATGAGAAATTAATGTTCTGCGG 668
DB 420 TAAAGAAATGCTGATGATGATGTTGAGAAATGAGAAATTAATGTTCTGCGG 479
QY 669 AATGAGGATTTGGCAATCTGCTGTTGCTGATGATCAATTCATCTGTGAGTA 728
DB 480 AATGAGGATTTGGCAATCTGCTGTTGCTGATGATCAATTCATCTGTGAGTA 539
QY 729 CTCTTTGACATGAGAAATTTCACTATATTCAAGCAAGCTAGGAATGTTCCCTTC 788
DB 540 CTCTTTGACATGAGAAATTTCACTATATTCAAGCAAGCTAGGAATGTTCCCTTC 599
QY 789 ACTGGGACCA 798
DB 600 ACTGGGACCA 609

```

RESULT 13
 DN997716 697 bp mRNA linear EST 17-MAY-2005
 LOCUS DN997716
 DEFINITION TC115356 Human breast cancer tissue, large insert, pcwv expression

1 library Homo sapiens cDNA clone TC115356 5' similar to Homo sapiens six transmembrane epithelial antigen of the prostate 1 (STEAP1), mRNA sequence.

ACCESSION DN997716.1 GI:66257543
 VERSION DN997716
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 697)
 Birkett,C., Cho,T., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,D., Wu,M., Zhang,X., Jay,G. and He,W.
 High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts
 Unpublished (2005)

JOURNAL
 COMMENT
 Contact: Kovacs, KF
 High Throughput cDNA Cloning
 Origene Technologies, Inc. (www.origene.com)
 6 Telt Court, Suite 100, Rockville, MD 20850, USA
 Tel: 301 340 3188
 Fax: 301 340 8606
 Email: CDNA@origene.com

This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc.
 Please contact Origene for access.

Origene Technologies, Inc.
 6 Telt Ct. Suite 100
 Rockville, MD 20850
 Tel: (301) 340-3188
 http://www.origene.com
 Seq primer: pcwv6 5prime forward vector primer, Origene Technologies Inc.

FEATURES

source

```

1..697
Location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TC115356"
/tissue_type="Breast cancer"
/clone_lib="Human breast cancer tissue, large insert, pcwv expression library"
/notes="Organ: Mammary gland (cancer tissue); Vector: pcwv6-XLS, Site 1: EcoRI, Site 2: XhoI/SalI compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts; cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"

```

ORIGIN

Query Match 58.8%; Score 598; DB 8; Length 697;
 Best Local Similarity 100.0%; Pred. No. 3.1e-148;
 Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGAAGAGAAAGACATCAACCAAGAACTTTGAAATTAAGAGCTAGAGA 60
DB 100 ATGGAAGAGAAAGACATCAACCAAGAACTTTGAAATTAAGAGAGCTAGAGA 159
QY 61 AATTTGAAGAAGACATTAATTTGCTAAGACACGGGAGAGACGATGCTAAAAA 120
DB 160 AATTTGAAGAAGACATTAATTTGCTAAGACACGGGAGAGACGATGCTAAAAA 219
QY 121 CCTGTGCTTTTCATTTGACCAACCAAGCCATGCTGATGAATTTGACTGCCCTT 180
DB 220 CCTGTGCTTTTCATTTGACCAACCAAGCCATGCTGATGAATTTGACTGCCCTT 279
QY 181 CTTCAGACACACAGAACTCTTTCCACAGTGGCACTTGGCAATTAATTAAGTCT 240
DB 280 CTTCAGACACACAGAACTCTTTCCACAGTGGCACTTGGCAATTAATTAAGTCT 339

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Qy	241	TTAGATGCTGACGCTTTCTTTTAACTCTTGAGGGAAAGTAATTAACCCCTTGGACACT	300
Db	340	ATAGATCTTGACTTCTTCTTAACTCTTGAGGGAAAGTAATTAACCCCTTGGACACT	399
Qy	301	TCCCATCAACATATTTTATTAATAATTCGAATCTGTCATCAACAAGTCCTGCCAATG	360
Db	400	TCCCATCAACATATTTTATTAATAATTCGAATCTGTCATCAACAAGTCCTGCCAATG	459
Qy	361	GTTTCGATCACTCTCTTGGAATGTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA	420
Db	460	GTTTCGATCACTCTCTTGGAATGTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA	519
Qy	421	CTTCATTAATGGAACCAAGTATTAAGAAGTTTCACATTTGGTGGATAGTGATGTATACA	480
Db	520	CTTCATTAATGGAACCAAGTATTAAGAAGTTTCACATTTGGTGGATAGTGATGTATACA	579
Qy	481	AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTGTGTGACGTGACATTCGAATTATAGTCTG	540
Db	580	AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTGTGTGACGTGACATTCGAATTATAGTCTG	639
Qy	541	TCTTACCCAATGAGGCGATCTCTACAGATPACAAGTGTCPAAACTGGGCAATATCAACAG	598
Db	640	TCTTACCCAATGAGGCGATCTCTACAGATPACAAGTGTCPAAACTGGGCAATATCAACAG	697

RESULT	14
LOCUS	BE881257
DEFINITION	BE881257 920 bp mRNA linear EST 20-OCT-2000 601492338r1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE3894657 5', mRNA sequence.
ACCESSION	BE881257
VERSION	BE881257.1 GI:10330033
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	1 (baaes 1 to 920)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM95684 row: k column: 10
 High quality sequence stop: 732.

FEATURES	Location/Qualifiers
Source	1. .920

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3894657"
/risuse_type="large cell carcinoma,
/ab_host="H10B (phase-resistant)"
/clone_id="NH_MGC_69
/notes="Organ: lung; Vector: PCMV-SpOrt6, Site_1: Not
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.1 kb. library constructed by
technologies."

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ORIGIN

Query Match	58.8%;	Score 597.8;	DB 2;	Length 920;
Best Local Similarity	93.4%;	Pred. No. 3.7e-148;		
Matches 724;	Conservative	0;	Mismatches 37;	Indels 14;
				Gaps 9;

138 GCACCAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAACTTCAGCACACACAGGA 197

Db	1	GCACCAACAGCCCATGCTGATGAATTTGAATCTGCGCTTCAGAACTTGACGACACACAGGA	60
QY	198	ACTCTTTCACAGTGGCACTTGGCAATTAAATAGCGCTAATTATACACTCTCGACTTT	257
Db	61	ACTCTTTCACAGTGGCACTTGGCAATTAAATAGCGCTAATTATACACTCTCGACTTT	120
QY	258	TCCTTACACTCTTCTGAGGGAAGTAATTCACCTTTAGCAACTTCCCATCAACATAATTT	317
Db	121	TCCTTACACTCTTCTGAGGGAAGTAATTCACCTTTAGCAACTTCCCATCAACATAATTT	180
QY	318	TTATTAATTCCTCAATCTCTGATCAACAAAGTCTTGCCAAATGGTTTCATCACTCTCTT	377
Db	181	TTATTAATTCCTCAATCTCTGATCAACAAAGTCTTGCCAAATGGTTTCATCACTCTCTT	240
QY	378	GGCAATGGTTTACCTGCGACGGTGTGATAGACGCAATGTCCAACTTCAATAGAACCA	437
Db	241	GGCA - TGGTTTACCTGCGACGGTGTGATAGACGCA - TGTCCAACTTCAATAGAACCA	298
QY	438	GTATTAAGAACTTCCACATTTGGTTGATTAAGTGAATGTTAACAAAGACAGTTTGGGCT	497
Db	299	GTATTAAGAACTTCCAC - TGGTTGAAATAGTGAATGTTAACAAAGACAG - TTTGGGCT	356
QY	498	TCTCAATTTCTTTTGTGCTGTAAGTGCATGCATGCAATTAATAGTGTCTTAACCAATAGAGCG	557
Db	357	TCTCAATTTCT - TTTTGTGCTGTAAGTGCATGCAATTAATAGTGTCTTAACCAATAGAGCG	415
QY	558	ATCCACAGATACAAAGTTGCTTAACTGGGCACTATCAACAGTCCAAACAAATTAAGAAGA	617
Db	416	ATCCACAGATACAAAGTTGCTTAACTGGGCACTATCAACAGGTCAAACAAATTAAGAAGA	475
QY	618	TGCGTGAATTAGGATGATTTTGGAGATGAGAAATTAATGTGTCTCTGGAAATTTGGG	677
Db	476	TGCGTGAATTAGGATGAT - TTGAGAAATGAGAAATTAATGTGTCTCTGGAAATTTGGG	534
QY	678	ATTGGCAATACTGCGCTGTGTGGCTGTGACACTATTCACATCTGAGTGAAGCTCTTGGAC	737
Db	535	ATTGGCAATACTGCGCTGTGTGGCTGTGACACTATTCACATCTGAGTGAAGCTCTTGGAC	594
QY	728	ATGAGAGAAATTCACATATTTACAGAGAACTAGGAATTTTTCCTTCACTAGGGGAC	797
Db	595	ATGAGAGAAATTCACATATTTACAGAGAACTAGGA - TGTGTCTCTTCACTAGGGGAC	653
QY	798	AATACAGCAATGGAATTTTGTGCTGGAATTAAGTGAATAGATATTAATAACAAATTTGATGTA	857
Db	654	AATACAGCAATGGAATTT - GGCTGGAATTAAGTGAATAGATATA - AACATTTGTGTA	706
QY	858	TACACTTCAACTTTATGATAGAGCTGTTTTCCTTCAATGTGTGCTCGAATATTT	912
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RESULT 15
CV757706

LOCUS	742 bp	mRNA	linear	EST	24-JAN-2005
AGENE					
DEFINITION	CX757709				
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	IMAGE:7772991	3'	mRNA	sequence.	

ACCESSION	CX757709	GI:58054365
VERSION	CX757709.1	
KEYWORDS	EST.	

SOURCE ORGANISM

REFERENCE
1 (bases 1 to 742)

REFERENCE 1 (bases 1 to 742)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC).
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.

National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-remail.nih.gov
 Tissue Procurement: Meri Firpo
 cDNA Library Preparation: Express Genomics
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov

Plate: L1AM15916 row: h column: 13
 High quality sequence start: 6
 High quality sequence stop: 726.

FEATURES

source

Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:7772991"
 /tissue_type="pluripotent cell line derived from
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 /lab_host="DH10B TONa"
 /clone_id="NIH MGC 278"
 /note="Organ: Blastocyst; Vector: pExpress-1; Site 1:
 EcoRV; Site 2: NotI; RNA obtained from pluripotent cell
 line derived from blastocyst inner cell mass (cell line
 HSF-1.14, NIH Registry designation UC01. Positive for OCT4
 expression by RT-PCR, positive for SSEA-3, SSEA-4,
 Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
 SSEA-1 by immunofluorescence. Passage 35. This line is a
 subclone of the parental line; the parental line was
 subcloned to remove aneuploid cells). cDNA was primed
 using oligo-dT primer:
 5'-pGACTGCTGCTGATCGCGCGCGCCGCC(Tr)25-3' and cloned into
 the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
 kb resulted in an average insert size of 1.9 kb. This
 primary library is non-normalized (normalized primary
 library is NIH_MGC_279) and was constructed by Express
 Genomics (Frederick, MD). Note: this is a Mammalian Gene
 Collection library."

ORIGIN

Query Match 58.6%; Score 596; DB 8; Length 742;
 Best Local Similarity 97.6%; Pred. No. 1,1e-147;

Matches 605; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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QY 1 ATGGAAGCAGAAAGACATCAACAACCAAGAACTTTGAAATGAAGCTTAGAGAGA 60
DB 123 ATGGAAGCAGAAAGACATCAACAACCAAGAAATTTGAAATGAAGCTTAGAGAGA 182
QY 61 AATTTAGAAGAGACGATTATTGTGATTAAGACACGAGAGACACGATGCTTAAAGA 120
DB 183 AATTTAGAAGAGACGATTATTGTGATTAAGACACGAGAGACACGATGCTTAAAGA 242
QY 121 CCTGTCCTTTTGTGATTCACCAACAGCCCATGCTGATGAATTTGACCTGCTTCA 180
DB 243 CCTGTCCTTTTGTGATTCACCAACAGCCCATGCTGATGAATTTGACCTGCTTCA 302
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DB 303 CTTGACACACACAGGACCTTTTGCACAGTGGCACTTGCCAAATTAATAGCTGCTATT 362
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DB 363 ATAGCATCTCTGACTTTTCTTACACTCTTCTGAGGGAAGTAATTCACCTTTAGCACT 422
QY 301 TCCCATCAACATATTTTATAAATTCATCTCTGATCATCAACAAAGCTTTGCGCATG 360
DB 423 TCCCATCAACATATTTTATAAATTCATCTCTGATCATCAACAAAGCTTTGCGCATG 482
QY 361 GTTTCATCACTCTCTTGGCATTGTTTACTGCGCAGGTGTGATGACAGCAATTTGCCAA 420
DB 483 GTTTCATCACTCTCTTGGCATTGTTTACTGCGCAGGTGTGATGACAGCAATTTGCCAA 542
QY 421 CTTCAATATGGAACCAAGTATTAAGATTTCACATTTGTTGATTAAGTATTAACA 480

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DB 543 CTTCAATATGGAACCAAGTATTAAGATTTCACATTTGTTGATTAAGTATTAACA 602
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QY 541 TCTTACCAATGAGGCGATCTTACAGATCAAGTTGCTTAACTGGGCATATCAACAGTTC 600
DB 663 TCTTACCAATGAGGCGATCTTACAGATCAAGTTGCTTAACTGGGCATATCAACAGTTC 722
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DB 723 CAACAAATTAAGAGATGC 742

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